GenCore version 5.1.6

OM protein - protein search, using sw model

Run on: January 13, 2005, 15:29:11 ; Search time 93 Seconds
(without alignments)
4366.468 Million cell updates/sec

Title: US-10-053-758-225
Perfect score: 5961
Sequence: 1 MPRAPRCRAVRSLLRSHYRE.....TALEAAANPALPSDFKTILD 1132

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 2002273 seqs, 358729299 residues

Total number of hits satisfying chosen parameters: 2002273

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : A_Geneseq_23Sep04:*
1: geneseqp1980s:*
2: geneseqp1990s:*
3: geneseqp2000s:*
4: geneseqp2001s:*
5: geneseqp2002s:*
6: geneseqp2003as:*
7: geneseqp2003bs:*
8: geneseqp2004s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	5961	100.0	1132	2	AAW46957	Aaw46957 Human tel
2	5961	100.0	1132	2	AAW90251	Aaw90251 Human cat
3	5961	100.0	1132	2	AAY28881	Aay28881 Human tel
4	5961	100.0	1132	2	AAY32090	Aay32090 Human tel
5	5961	100.0	1132	2	AAY43621	Aay43621 A human t
6	5961	100.0	1132	2	AAY26580	Aay26580 Human tel
7	5961	100.0	1132	4	AAG64859	Aag64859 Heart mus
8	5961	100.0	1132	4	AAG64329	Aag64329 Human pro
9	5961	100.0	1132	4	AAB99930	Aab99930 Human tel
10	5961	100.0	1132	4	AAB82765	Aab82765 Human tel
11	5961	100.0	1132	5	AAE29226	Aae29226 Human tel
12	5961	100.0	1132	5	AAU72735	Aau72735 Human tel
13	5961	100.0	1132	6	ABR42384	Abr42384 Human tel
14	5961	100.0	1132	6	ABR42063	Abr42063 Human tel
15	5961	100.0	1132	6	ABP56676	Abp56676 Human tel
16	5961	100.0	1132	6	ABR58045	Abr58045 Human tel
17	5961	100.0	1132	7	ADD21420	Add21420 Human TER
18	5961	100.0	1132	7	ADH72743	Adh72743 Human pro
19	5961	100.0	1132	8	ADG70114	Adg70114 hTERT pro
20	5961	100.0	1132	8	ADG90599	Adg90599 Human TER
21	5961	100.0	1132	8	ADI82172	Adi82172 Human tel
22	5961	100.0	1154	2	AAW61350	Aaw61350 Human tel
23	5961	100.0	1189	2	AAW47008	Aaw47008 Glutathio
24	5955	99.9	1285	2	AAW47000	Aaw47000 HIS tagge
25	5954	99.9	1132	2	AAW71376	Aaw71376 Human tel
26	5954	99.9	1132	2	AAY00627	Aay00627 Human tel
27	5954	99.9	1132	2	AAY00638	Aay00638 Truncated
28	5954	99.9	1132	2	AAY28401	Aay28401 Human EST
29	5954	99.9	1132	3	AAY96566	Aay96566 hEST2, a
30	5954	99.9	1132	7	ADC47061	Adc47061 Human TER
31	5954	99.9	1132	7	ADE40482	Ade40482 Human tel
32	5952	99.8	1132	2	AAW56113	Aaw56113 Human tel
33	5927	99.4	1166	2	AAY00647	Aay00647 Telomeras
34	5918	99.3	1405	2	AAW56101	Aaw56101 Enhanced
35	5911.5	99.2	1199	2	AAW47007	Aaw47007 Glutathio
36	5882	98.7	1120	2	AAY00641	Aay00641 Telomeras
37	5873	98.5	1120	2	AAY00650	Aay00650 Telomeras
38	5721	96.0	1150	2	AAW47006	Aaw47006 Glutathio
39	5555	93.2	1053	2	AAY00640	Aay00640 Altered C
40	5516	92.5	1093	2	AAY00649	Aay00649 Altered C
41	5467	91.7	1041	2	AAY00652	Aay00652 Altered C
42	5467	91.7	1041	2	AAY00643	Aay00643 Altered C
43	5008	84.0	948	2	AAY00639	Aay00639 N-termina
44	5004	83.9	948	2	AAY00648	Aay00648 Truncated
45	4932	82.7	936	2	AAY00642	Aay00642 Truncated

ALIGNMENTS

RESULT 1
AAW46957
ID AAW46957 standard; protein; 1132 AA.
XX
AC AAW46957;
XX
DT 13-AUG-1998 (first entry)
XX
DE Human telomerase reverse transcriptase.
XX
KW Human; telomerase reverse transcriptase; hTRT; TRT; diagnosis; prognosis;
KW cell proliferation; cancer; ageing; ribonucleoprotein.
XX
OS Homo sapiens.
XX
PN GB2317891-A.
XX
PD 08-APR-1998.
XX
PF 01-OCT-1997; 97GB-00020890.
XX
PR 01-OCT-1996; 96US-00724643.
PR 18-APR-1997; 97US-00844419.
PR 25-APR-1997; 97US-00846017.
PR 06-MAY-1997; 97US-00851843.
PR 09-MAY-1997; 97US-00854050.
PR 14-AUG-1997; 97US-00911312.
PR 14-AUG-1997; 97US-00912951.
PR 14-AUG-1997; 97US-00915503.
XX
PA (GERO-) GERON CORP.
PA (UYTE-) UNIV TECHNOLOGY CORP.
XX
PI Cech TR, Lingner J, Nakamura T, Chapman KB, Morin GB, Harley CB;
PI Andrews WH;
XX
DR WPI; 1998-171633/16.
DR N-PSDB; AAV22379.
XX
PT Pure and recombinant human Telomerase Reverse Transcriptase and its
PT variants - are useful in the diagnosis, prognosis and treatment of cell
PT proliferation conditions especially cancer and ageing.
XX
PS Claim 3; Fig 17; 387pp; English.
XX
CC The present sequence represents human telomerase reverse transcriptase
CC (hTRT), which is a ribonucleoprotein. The present invention also
CC describes the following methods: (A) determining whether a test compound

CC is a modulator of hTRT, by detecting the change in hTRT recombinant
CC protein or polynucleotide, on administration of the compound; (B)
CC preparation of recombinant telomerase by contacting a protein preparation
CC of hTRT with a telomerase RNA component; (C) detection of the hTRT RNA or
CC protein in a sample by binding a relevant probe to the sample and
CC detecting the complex formed or in the case of RNA detection, amplifying
CC the product and correlating the presence of complex or amplification
CC product with presence of hTRT in the sample; and (D) increasing the
CC proliferation of a vertebrate cell by increasing hTRT expression; and (E)
CC the use of an agent that causes an increase in cell vertebrate cell
CC proliferation to create a medicament that inhibits ageing. A protein
CC preparation of hTRT and the polynucleotide encoding hTRT can be used in
CC the manufacture of medicaments for inhibiting the effect of ageing or
CC cancer. Inhibitors of telomerase activity can be used to treat conditions
CC that are associated with high telomerase activity. A protein preparation
CC of hTRT can also be used in the new methods
XX
SQ Sequence 1132 AA;

Query Match 100.0%; Score 5961; DB 2; Length 1132;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1132; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy          1 MPRAPRCRAVRSLLRSHYREVLPLATFVRRLGPQGWRLVQRGDPAAFRALVAQCLVCVPW 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 MPRAPRCRAVRSLLRSHYREVLPLATFVRRLGPQGWRLVQRGDPAAFRALVAQCLVCVPW 60

Qy         61 DARPPPAAPSFRQVSCLKELVARVLQRLCERGAKNVLAFGFALLDGARGGPPEAFTTSVR 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 DARPPPAAPSFRQVSCLKELVARVLQRLCERGAKNVLAFGFALLDGARGGPPEAFTTSVR 120

Qy        121 SYLPNTVTDALRGSGAWGLLLRRVGDDVLVHLLARCALFVLVAPSCAYQVCGPPLYQLGA 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 SYLPNTVTDALRGSGAWGLLLRRVGDDVLVHLLARCALFVLVAPSCAYQVCGPPLYQLGA 180

Qy        181 ATQARPPPHASGPRRRLGCERAWNHSVREAGVPLGLPAPGARRRGGSASRSLPLPKRPRR 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 ATQARPPPHASGPRRRLGCERAWNHSVREAGVPLGLPAPGARRRGGSASRSLPLPKRPRR 240

Qy        241 GAAPEPERTPVGQGSWAHPGRTRGPSDRGFCVVSPARPAEEATSLEGALSGTRHSHPSVG 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 GAAPEPERTPVGQGSWAHPGRTRGPSDRGFCVVSPARPAEEATSLEGALSGTRHSHPSVG 300

Qy        301 RQHHAGPPSTSRPPRPWDTPCPPVYAETKHFLYSSGDKEQLRPSFLLSSLRPSLTGARRL 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 RQHHAGPPSTSRPPRPWDTPCPPVYAETKHFLYSSGDKEQLRPSFLLSSLRPSLTGARRL 360

Qy        361 VETIFLGSRPWMPGTPRRLPRLPQRYWQMRPLFLELLGNHAQCPYGVLLKTHCPLRAAVT 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        361 VETIFLGSRPWMPGTPRRLPRLPQRYWQMRPLFLELLGNHAQCPYGVLLKTHCPLRAAVT 420

Qy        421 PAAGVCAREKPQGSVAAPEEEDTDPRRLVQLLRQHSSPWQVYGFVRACLRRLVPPGLWGS 480
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        421 PAAGVCAREKPQGSVAAPEEEDTDPRRLVQLLRQHSSPWQVYGFVRACLRRLVPPGLWGS 480

Qy        481 RHNERRFLRNTKKFISLGKHAKLSLQELTWKMSVRDCAWLRRSPGVGCVPAAEHRLREEI 540
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        481 RHNERRFLRNTKKFISLGKHAKLSLQELTWKMSVRDCAWLRRSPGVGCVPAAEHRLREEI 540

Qy        541 LAKFLHWLMSVYVVELLRSFFYVTETTFQKNRLFFYRKSVWSKLQSIGIRQHLKRVQLRE 600
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        541 LAKFLHWLMSVYVVELLRSFFYVTETTFQKNRLFFYRKSVWSKLQSIGIRQHLKRVQLRE 600

Qy        601 LSEAEVRQHREARPALLTSRLRFIPKPDGLRPIVNMDYVVGARTFRREKRAERLTSRVKA 660
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        601 LSEAEVRQHREARPALLTSRLRFIPKPDGLRPIVNMDYVVGARTFRREKRAERLTSRVKA 660

Qy        661 LFSVLNYERARRPGLLGASVLGLDDIHRAWRTFVLRVRAQDPPPELYFVKVDVTGAYDTI 720
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        661 LFSVLNYERARRPGLLGASVLGLDDIHRAWRTFVLRVRAQDPPPELYFVKVDVTGAYDTI 720

Qy        721 PQDRLTEVIASIIKPQNTYCVRRYAVVQKAAHGHVRKAFKSHVSTLTDLQPYMRQFVAHL 780
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        721 PQDRLTEVIASIIKPQNTYCVRRYAVVQKAAHGHVRKAFKSHVSTLTDLQPYMRQFVAHL 780

Qy        781 QETSPLRDAVVIEQSSSLNEASSGLFDVFLRFMCHHAVRIRGKSYVQCQGIPQGSILSTL 840
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        781 QETSPLRDAVVIEQSSSLNEASSGLFDVFLRFMCHHAVRIRGKSYVQCQGIPQGSILSTL 840

Qy        841 LCSLCYGDMENKLFAGIRRDGLLLRLVDDFLLVTPHLTHAKTFLRTLVRGVPEYGCVVNL 900
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        841 LCSLCYGDMENKLFAGIRRDGLLLRLVDDFLLVTPHLTHAKTFLRTLVRGVPEYGCVVNL 900

Qy        901 RKTVVNFPVEDEALGGTAFVQMPAHGLFPWCGLLLDTRTLEVQSDYSSYARTSIRASLTF 960
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        901 RKTVVNFPVEDEALGGTAFVQMPAHGLFPWCGLLLDTRTLEVQSDYSSYARTSIRASLTF 960

Qy        961 NRGFKAGRNMRRKLFGVLRLKCHSLFLDLQVNSLQTVCTNIYKILLLQAYRFHACVLQLP 1020
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        961 NRGFKAGRNMRRKLFGVLRLKCHSLFLDLQVNSLQTVCTNIYKILLLQAYRFHACVLQLP 1020

Qy       1021 FHQQVWKNPTFFLRVISDTASLCYSILKAKNAGMSLGAKGAAGPLPSEAVQWLCHQAFLL 1080
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1021 FHQQVWKNPTFFLRVISDTASLCYSILKAKNAGMSLGAKGAAGPLPSEAVQWLCHQAFLL 1080

Qy       1081 KLTRHRVTYVPLLGSLRTAQTQLSRKLPGTTLTALEAAANPALPSDFKTILD 1132
              |||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1081 KLTRHRVTYVPLLGSLRTAQTQLSRKLPGTTLTALEAAANPALPSDFKTILD 1132
```

RESULT 2
AAW90251
ID AAW90251 standard; protein; 1132 AA.
XX
AC AAW90251;
XX
DT 24-MAY-1999 (first entry)
XX
DE Human catalytic telomerase sub-unit protein.
XX
KW Human; catalytic telomerase subunit; therapy; diagnosis; hTC; assay;
KW modulator; treatment; inhibit; cellular disorder; death; defect; cancer;
KW ageing; antisense; neoplastic cell; telomerase-related condition;
KW tumour cell.
XX
OS Homo sapiens.
XX
PN WO9859040-A2.
XX
PD 30-DEC-1998.
XX
PF 09-JUN-1998; 98WO-EP003468.
XX
PR 20-JUN-1997; 97DE-01026329.
PR 26-MAR-1998; 98DE-01013274.
PR 14-APR-1998; 98DE-01016496.
XX
PA (FARB) BAYER AG.
XX
PI Hagen G, Siegmund H, Weichel W, Wick M, Zubov D;
XX
DR WPI; 1999-081276/07.
DR N-PSDB; AAV72117.
XX
PT New catalytically active subunit of human telomerase - used in the
PT modulation of telomerase activity, particularly for treating cancer and
PT ageing.
XX
PS Claim 2; Fig 2; 76pp; German.
XX
CC This sequence represents a novel human catalytic telomerase sub-unit
CC (hTC). This protein can be used in screening assays to identify
CC modulators of telomerase and to treat or inhibit cellular disorders,
CC death, defects and/or other pathological processes involving telomerase,
CC particularly cancer and ageing (also suitable for this are agents that
CC stimulate, inhibit or mimic the activity of the subunit). Antisense

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CC   nucleic acids inhibit telomerase action (by binding to specific mRNA),
CC   particularly in neoplastic cells and may be expressed in vivo. Antibodies
CC   and fragments of the protein, used as probes or primers, are used to
CC   diagnose telomerase-related conditions (especially neoplasia) by (i)
CC   detecting abnormal levels of the subunit protein in body fluids or
CC   tissues or (ii) by measuring the amount of the encoding nucleic acid.
CC   Expression of the nucleic acid encoding the subunit mRNA is confined to
CC   tumour cells, in contrast to the ubiquitous expression of the telomerase
CC   RNA subunit
XX
SQ   Sequence 1132 AA;

  Query Match             100.0%;  Score 5961;  DB 2;  Length 1132;
  Best Local Similarity   100.0%;  Pred. No. 0;
  Matches 1132;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 MPRAPRCRAVRSLLRSHYREVLPLATFVRRLGPQGWRLVQRGDPAAFRALVAQCLVCVPW 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 MPRAPRCRAVRSLLRSHYREVLPLATFVRRLGPQGWRLVQRGDPAAFRALVAQCLVCVPW 60

Qy         61 DARPPPAAPSFRQVSCLKELVARVLQRLCERGAKNVLAFGFALLDGARGGPPEAFTTSVR 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 DARPPPAAPSFRQVSCLKELVARVLQRLCERGAKNVLAFGFALLDGARGGPPEAFTTSVR 120

Qy        121 SYLPNTVTDALRGSGAWGLLLRRVGDDVLVHLLARCALFVLVAPSCAYQVCGPPLYQLGA 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 SYLPNTVTDALRGSGAWGLLLRRVGDDVLVHLLARCALFVLVAPSCAYQVCGPPLYQLGA 180

Qy        181 ATQARPPPHASGPRRRLGCERAWNHSVREAGVPLGLPAPGARRRGGSASRSLPLPKRPRR 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 ATQARPPPHASGPRRRLGCERAWNHSVREAGVPLGLPAPGARRRGGSASRSLPLPKRPRR 240

Qy        241 GAAPEPERTPVGQGSWAHPGRTRGPSDRGFCVVSPARPAEEATSLEGALSGTRHSHPSVG 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 GAAPEPERTPVGQGSWAHPGRTRGPSDRGFCVVSPARPAEEATSLEGALSGTRHSHPSVG 300

Qy        301 RQHHAGPPSTSRPPRPWDTPCPPVYAETKHFLYSSGDKEQLRPSFLLSSLRPSLTGARRL 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 RQHHAGPPSTSRPPRPWDTPCPPVYAETKHFLYSSGDKEQLRPSFLLSSLRPSLTGARRL 360

Qy        361 VETIFLGSRPWMPGTPRRLPRLPQRYWQMRPLFLELLGNHAQCPYGVLLKTHCPLRAAVT 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        361 VETIFLGSRPWMPGTPRRLPRLPQRYWQMRPLFLELLGNHAQCPYGVLLKTHCPLRAAVT 420

Qy        421 PAAGVCAREKPQGSVAAPEEEDTDPRRLVQLLRQHSSPWQVYGFVRACLRRLVPPGLWGS 480
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        421 PAAGVCAREKPQGSVAAPEEEDTDPRRLVQLLRQHSSPWQVYGFVRACLRRLVPPGLWGS 480

Qy        481 RHNERRFLRNTKKFISLGKHAKLSLQELTWKMSVRDCAWLRRSPGVGCVPAAEHRLREEI 540
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        481 RHNERRFLRNTKKFISLGKHAKLSLQELTWKMSVRDCAWLRRSPGVGCVPAAEHRLREEI 540

Qy        541 LAKFLHWLMSVYVVELLRSFFYVTETTFQKNRLFFYRKSVWSKLQSIGIRQHLKRVQLRE 600
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        541 LAKFLHWLMSVYVVELLRSFFYVTETTFQKNRLFFYRKSVWSKLQSIGIRQHLKRVQLRE 600

Qy        601 LSEAEVRQHREARPALLTSRLRFIPKPDGLRPIVNMDYVVGARTFRREKRAERLTSRVKA 660
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        601 LSEAEVRQHREARPALLTSRLRFIPKPDGLRPIVNMDYVVGARTFRREKRAERLTSRVKA 660

Qy        661 LFSVLNYERARRPGLLGASVLGLDDIHRAWRTFVLRVRAQDPPPELYFVKVDVTGAYDTI 720
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        661 LFSVLNYERARRPGLLGASVLGLDDIHRAWRTFVLRVRAQDPPPELYFVKVDVTGAYDTI 720

Qy        721 PQDRLTEVIASIIKPQNTYCVRRYAVVQKAAHGHVRKAFKSHVSTLTDLQPYMRQFVAHL 780
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        721 PQDRLTEVIASIIKPQNTYCVRRYAVVQKAAHGHVRKAFKSHVSTLTDLQPYMRQFVAHL 780

Qy        781 QETSPLRDAVVIEQSSSLNEASSGLFDVFLRFMCHHAVRIRGKSYVQCQGIPQGSILSTL 840
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        781 QETSPLRDAVVIEQSSSLNEASSGLFDVFLRFMCHHAVRIRGKSYVQCQGIPQGSILSTL 840

Qy        841 LCSLCYGDMENKLFAGIRRDGLLLRLVDDFLLVTPHLTHAKTFLRTLVRGVPEYGCVVNL 900
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        841 LCSLCYGDMENKLFAGIRRDGLLLRLVDDFLLVTPHLTHAKTFLRTLVRGVPEYGCVVNL 900

Qy        901 RKTVVNFPVEDEALGGTAFVQMPAHGLFPWCGLLLDTRTLEVQSDYSSYARTSIRASLTF 960
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        901 RKTVVNFPVEDEALGGTAFVQMPAHGLFPWCGLLLDTRTLEVQSDYSSYARTSIRASLTF 960

Qy        961 NRGFKAGRNMRRKLFGVLRLKCHSLFLDLQVNSLQTVCTNIYKILLLQAYRFHACVLQLP 1020
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        961 NRGFKAGRNMRRKLFGVLRLKCHSLFLDLQVNSLQTVCTNIYKILLLQAYRFHACVLQLP 1020

Qy       1021 FHQQVWKNPTFFLRVISDTASLCYSILKAKNAGMSLGAKGAAGPLPSEAVQWLCHQAFLL 1080
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1021 FHQQVWKNPTFFLRVISDTASLCYSILKAKNAGMSLGAKGAAGPLPSEAVQWLCHQAFLL 1080

Qy       1081 KLTRHRVTYVPLLGSLRTAQTQLSRKLPGTTLTALEAAANPALPSDFKTILD 1132
              ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1081 KLTRHRVTYVPLLGSLRTAQTQLSRKLPGTTLTALEAAANPALPSDFKTILD 1132


RESULT 3
AAY28881
ID   AAY28881 standard; protein; 1132 AA.
XX
AC   AAY28881;
XX
DT   17-JAN-2000  (first entry)
XX
DE   Human telomerase reverse transcriptase protein.
XX
KW   Human telomerase reverse transcriptase protein; hTRT; telomerase; hEST2;
KW   catalytic protein component; cell proliferative capacity; DNA primer;
KW   telomerase substrate; telomeric DNA synthesis; cell immortality;
KW   neoplastic phenotype; diagnostic application; prognostic application;
KW   telomerase related condition; cancer; therapeutic agent;
KW   telomerase expression; telomerase activity.
XX
OS   Homo sapiens.
XX
FH   Key             Location/Qualifiers
FT   Misc-difference 608
FT                   /note= "Corresponds to cac codon"
XX
PN   WO9950279-A1.
XX
PD   07-OCT-1999.
XX
PF   31-MAR-1999;   99WO-US007160.
XX
PR   31-MAR-1998;   98US-00052919.
XX
PA   (GERO-) GERON CORP.
PA   (UYTE-) UNIV TECHNOLOGY CORP.
XX
PI   Cech TR,  Lingner J,  Nakamura T,  Chapman KB,  Morin GB,  Harley CB;
PI   Andrews WH;
XX
DR   WPI; 1999-610834/52.
DR   N-PSDB; AAZ08150.
XX
PT   Antisense polynucleotides for human telomerase reverse transcriptase used
PT   for diagnosing or treating cancer.
XX
PS   Claim 2; Fig 2; 31pp; English.
XX
CC   The present sequence is human telomerase reverse transcriptase protein.
CC   This is the catalytic protein component of telomerase and is also
CC   referred to as hEST2. HTRT has the ability to extend a DNA primer that
CC   functions as a telomerase substrate for telomeric DNA synthesis. This
CC   correlates with cell proliferative capacity, cell immortality, and the
CC   development of a neoplastic phenotype. Human TRT antisense
CC   oligonucleotides are useful for diagnostic or prognostic applications to
CC   telomerase related conditions, including cancer. They are also useful as
```

CC therapeutic agents, for inhibition of telomerase expression and activity
XX
SQ Sequence 1132 AA;

Query Match 100.0%; Score 5961; DB 2; Length 1132;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1132; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```
Qy          1 MPRAPRCRAVRSLLRSHYREVLPLATFVRRLGPQGWRLVQRGDPAAFRALVAQCLVCVPW 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 MPRAPRCRAVRSLLRSHYREVLPLATFVRRLGPQGWRLVQRGDPAAFRALVAQCLVCVPW 60

Qy         61 DARPPPAAPSFRQVSCLKELVARVLQRLCERGAKNVLAFGFALLDGARGGPPEAFTTSVR 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 DARPPPAAPSFRQVSCLKELVARVLQRLCERGAKNVLAFGFALLDGARGGPPEAFTTSVR 120

Qy        121 SYLPNTVTDALRGSGAWGLLLRRVGDDVLVHLLARCALFVLVAPSCAYQVCGPPLYQLGA 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 SYLPNTVTDALRGSGAWGLLLRRVGDDVLVHLLARCALFVLVAPSCAYQVCGPPLYQLGA 180

Qy        181 ATQARPPPHASGPRRRLGCERAWNHSVREAGVPLGLPAPGARRRGGSASRSLPLPKRPRR 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 ATQARPPPHASGPRRRLGCERAWNHSVREAGVPLGLPAPGARRRGGSASRSLPLPKRPRR 240

Qy        241 GAAPEPERTPVGQGSWAHPGRTRGPSDRGFCVVSPARPAEEATSLEGALSGTRHSHPSVG 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 GAAPEPERTPVGQGSWAHPGRTRGPSDRGFCVVSPARPAEEATSLEGALSGTRHSHPSVG 300

Qy        301 RQHHAGPPSTSRPPRPWDTPCPPVYAETKHFLYSSGDKEQLRPSFLLSSLRPSLTGARRL 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 RQHHAGPPSTSRPPRPWDTPCPPVYAETKHFLYSSGDKEQLRPSFLLSSLRPSLTGARRL 360

Qy        361 VETIFLGSRPWMPGTPRRLPRLPQRYWQMRPLFLELLGNHAQCPYGVLLKTHCPLRAAVT 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        361 VETIFLGSRPWMPGTPRRLPRLPQRYWQMRPLFLELLGNHAQCPYGVLLKTHCPLRAAVT 420

Qy        421 PAAGVCAREKPQGSVAAPEEEDTDPRRLVQLLRQHSSPWQVYGFVRACLRRLVPPGLWGS 480
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        421 PAAGVCAREKPQGSVAAPEEEDTDPRRLVQLLRQHSSPWQVYGFVRACLRRLVPPGLWGS 480

Qy        481 RHNERRFLRNTKKFISLGKHAKLSLQELTWKMSVRDCAWLRRSPGVGCVPAAEHRLREEI 540
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        481 RHNERRFLRNTKKFISLGKHAKLSLQELTWKMSVRDCAWLRRSPGVGCVPAAEHRLREEI 540

Qy        541 LAKFLHWLMSVYVVELLRSFFYVTETTFQKNRLFFYRKSVWSKLQSIGIRQHLKRVQLRE 600
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        541 LAKFLHWLMSVYVVELLRSFFYVTETTFQKNRLFFYRKSVWSKLQSIGIRQHLKRVQLRE 600

Qy        601 LSEAEVRQHREARPALLTSRLRFIPKPDGLRPIVNMDYVVGARTFRREKRAERLTSRVKA 660
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        601 LSEAEVRQHREARPALLTSRLRFIPKPDGLRPIVNMDYVVGARTFRREKRAERLTSRVKA 660

Qy        661 LFSVLNYERARRPGLLGASVLGLDDIHRAWRTFVLRVRAQDPPPELYFVKVDVTGAYDTI 720
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        661 LFSVLNYERARRPGLLGASVLGLDDIHRAWRTFVLRVRAQDPPPELYFVKVDVTGAYDTI 720

Qy        721 PQDRLTEVIASIIKPQNTYCVRRYAVVQKAAHGHVRKAFKSHVSTLTDLQPYMRQFVAHL 780
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        721 PQDRLTEVIASIIKPQNTYCVRRYAVVQKAAHGHVRKAFKSHVSTLTDLQPYMRQFVAHL 780

Qy        781 QETSPLRDAVVIEQSSSLNEASSGLFDVFLRFMCHHAVRIRGKSYVQCQGIPQGSILSTL 840
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        781 QETSPLRDAVVIEQSSSLNEASSGLFDVFLRFMCHHAVRIRGKSYVQCQGIPQGSILSTL 840

Qy        841 LCSLCYGDMENKLFAGIRRDGLLLRLVDDFLLVTPHLTHAKTFLRTLVRGVPEYGCVVNL 900
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        841 LCSLCYGDMENKLFAGIRRDGLLLRLVDDFLLVTPHLTHAKTFLRTLVRGVPEYGCVVNL 900

Qy        901 RKTVVNFPVEDEALGGTAFVQMPAHGLFPWCGLLLDTRTLEVQSDYSSYARTSIRASLTF 960
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        901 RKTVVNFPVEDEALGGTAFVQMPAHGLFPWCGLLLDTRTLEVQSDYSSYARTSIRASLTF 960

Qy        961 NRGFKAGRNMRRKLFGVLRLKCHSLFLDLQVNSLQTVCTNIYKILLLQAYRFHACVLQLP 1020
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        961 NRGFKAGRNMRRKLFGVLRLKCHSLFLDLQVNSLQTVCTNIYKILLLQAYRFHACVLQLP 1020

Qy       1021 FHQQVWKNPTFFLRVISDTASLCYSILKAKNAGMSLGAKGAAGPLPSEAVQWLCHQAFLL 1080
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1021 FHQQVWKNPTFFLRVISDTASLCYSILKAKNAGMSLGAKGAAGPLPSEAVQWLCHQAFLL 1080

Qy       1081 KLTRHRVTYVPLLGSLRTAQTQLSRKLPGTTLTALEAAANPALPSDFKTILD 1132
              ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1081 KLTRHRVTYVPLLGSLRTAQTQLSRKLPGTTLTALEAAANPALPSDFKTILD 1132
```

RESULT 4
AAY32090
ID AAY32090 standard; protein; 1132 AA.
XX
AC AAY32090;
XX
DT 17-JAN-2000 (first entry)
XX
DE Human telomerase reverse transcriptase (hTRT).
XX
KW Telomerase reverse transcriptase; human; hTRT; cell proliferation;
KW cancer.
XX
OS Homo sapiens.
XX
PN WO9950386-A2.
XX
PD 07-OCT-1999.
XX
PF 31-MAR-1999; 99WO-US007097.
XX
PR 31-MAR-1998; 98US-00052864.
PR 03-AUG-1998; 98US-00128354.
XX
PA (GERO-) GERON CORP.
XX
PI Morin GB;
XX
DR WPI; 1999-610842/52.
DR N-PSDB; AAZ20279.
XX
PT New catalytic polypeptide and polynucleotide, useful for increasing
PT catalytic activity in a cell.
XX
PS Claim 13; Fig 1; 24pp; English.
XX
CC The present sequence represents human telomerase reverse transcriptase
CC (hTRT). Human telomerase is a target for diagnosing and treating diseases
CC relating to cell proliferation and senescence, such as cancer, or for
CC increasing the proliferative capacity of a cell. A claimed method for
CC increasing the proliferative capacity of a vertebrate cell, especially a
CC human or other mammalian cell, involves introducing into the cell a
CC recombinant hTRT polynucleotide encoding an hTRT variant in which
CC residues 192-323, 200-323, 192-271, 200-271, 222-240, 415-450, 192-323
CC and 415-450, or 192-271 and 415-450 of the present sequence are deleted.
CC A claimed method of preparing recombinant telomerase involves contacting
CC a recombinant hTRT deletion mutant (as above) with a telomerase RNA
CC component such that the 2 proteins associate to form a complex capable of
CC catalysing the addition of nucleotides to a telomerase substrate. A
CC claimed method for reducing telomerase activity in a cell involves
CC introducing a recombinant polynucleotide encoding an hTRT variant having
CC a deletion of amino acids 192-450, 560-565, 637-660, 638-660, 748-764 or
CC 1055-1071 of the present sequence
XX
SQ Sequence 1132 AA;

Query Match 100.0%; Score 5961; DB 2; Length 1132;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1132; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```
Qy          1 MPRAPRCRAVRSLLRSHYREVLPLATFVRRLGPQGWRLVQRGDPAAFRALVAQCLVCVPW 60
```

```
Db          1 MPRAPRCRAVRSLLRSHYREVLPLATFVRRLGPQGWRLVQRGDPAAFRALVAQCLVCVPW 60

Qy         61 DARPPPAAPSFRQVSCLKELVARVLQRLCERGAKNVLAFGFALLDGARGGPPEAFTTSVR 120

Db         61 DARPPPAAPSFRQVSCLKELVARVLQRLCERGAKNVLAFGFALLDGARGGPPEAFTTSVR 120

Qy        121 SYLPNTVTDALRGSGAWGLLLRRVGDDVLVHLLARCALFVLVAPSCAYQVCGPPLYQLGA 180

Db        121 SYLPNTVTDALRGSGAWGLLLRRVGDDVLVHLLARCALFVLVAPSCAYQVCGPPLYQLGA 180

Qy        181 ATQARPPPHASGPRRRLGCERAWNHSVREAGVPLGLPAPGARRRGGSASRSLPLPKRPRR 240

Db        181 ATQARPPPHASGPRRRLGCERAWNHSVREAGVPLGLPAPGARRRGGSASRSLPLPKRPRR 240

Qy        241 GAAPEPERTPVGQGSWAHPGRTRGPSDRGFCVVSPARPAEEATSLEGALSGTRHSHPSVG 300

Db        241 GAAPEPERTPVGQGSWAHPGRTRGPSDRGFCVVSPARPAEEATSLEGALSGTRHSHPSVG 300

Qy        301 RQHHAGPPSTSRPPRPWDTPCPPVYAETKHFLYSSGDKEQLRPSFLLSSLRPSLTGARRL 360

Db        301 RQHHAGPPSTSRPPRPWDTPCPPVYAETKHFLYSSGDKEQLRPSFLLSSLRPSLTGARRL 360

Qy        361 VETIFLGSRPWMPGTPRRLPRLPQRYWQMRPLFLELLGNHAQCPYGVLLKTHCPLRAAVT 420

Db        361 VETIFLGSRPWMPGTPRRLPRLPQRYWQMRPLFLELLGNHAQCPYGVLLKTHCPLRAAVT 420

Qy        421 PAAGVCAREKPQGSVAAPEEEDTDPRRLVQLLRQHSSPWQVYGFVRACLRRLVPPGLWGS 480

Db        421 PAAGVCAREKPQGSVAAPEEEDTDPRRLVQLLRQHSSPWQVYGFVRACLRRLVPPGLWGS 480

Qy        481 RHNERRFLRNTKKFISLGKHAKLSLQELTWKMSVRDCAWLRRSPGVGCVPAAEHRLREEI 540

Db        481 RHNERRFLRNTKKFISLGKHAKLSLQELTWKMSVRDCAWLRRSPGVGCVPAAEHRLREEI 540

Qy        541 LAKFLHWLMSVYVVELLRSFFYVTETTFQKNRLFFYRKSVWSKLQSIGIRQHLKRVQLRE 600

Db        541 LAKFLHWLMSVYVVELLRSFFYVTETTFQKNRLFFYRKSVWSKLQSIGIRQHLKRVQLRE 600

Qy        601 LSEAEVRQHREARPALLTSRLRFIPKPDGLRPIVNMDYVVGARTFRREKRAERLTSRVKA 660

Db        601 LSEAEVRQHREARPALLTSRLRFIPKPDGLRPIVNMDYVVGARTFRREKRAERLTSRVKA 660

Qy        661 LFSVLNYERARRPGLLGASVLGLDDIHRAWRTFVLRVRAQDPPPELYFVKVDVTGAYDTI 720

Db        661 LFSVLNYERARRPGLLGASVLGLDDIHRAWRTFVLRVRAQDPPPELYFVKVDVTGAYDTI 720

Qy        721 PQDRLTEVIASIIKPQNTYCVRRYAVVQKAAHGHVRKAFKSHVSTLTDLQPYMRQFVAHL 780

Db        721 PQDRLTEVIASIIKPQNTYCVRRYAVVQKAAHGHVRKAFKSHVSTLTDLQPYMRQFVAHL 780

Qy        781 QETSPLRDAVVIEQSSSLNEASSGLFDVFLRFMCHHAVRIRGKSYVQCQGIPQGSILSTL 840

Db        781 QETSPLRDAVVIEQSSSLNEASSGLFDVFLRFMCHHAVRIRGKSYVQCQGIPQGSILSTL 840

Qy        841 LCSLCYGDMENKLFAGIRRDGLLLRLVDDFLLVTPHLTHAKTFLRTLVRGVPEYGCVVNL 900

Db        841 LCSLCYGDMENKLFAGIRRDGLLLRLVDDFLLVTPHLTHAKTFLRTLVRGVPEYGCVVNL 900

Qy        901 RKTVVNFPVEDEALGGTAFVQMPAHGLFPWCGLLLDTRTLEVQSDYSSYARTSIRASLTF 960

Db        901 RKTVVNFPVEDEALGGTAFVQMPAHGLFPWCGLLLDTRTLEVQSDYSSYARTSIRASLTF 960

Qy        961 NRGFKAGRNMRRKLFGVLRLKCHSLFLDLQVNSLQTVCTNIYKILLLQAYRFHACVLQLP 1020

Db        961 NRGFKAGRNMRRKLFGVLRLKCHSLFLDLQVNSLQTVCTNIYKILLLQAYRFHACVLQLP 1020

Qy       1021 FHQQVWKNPTFFLRVISDTASLCYSILKAKNAGMSLGAKGAAGPLPSEAVQWLCHQAFLL 1080

Db       1021 FHQQVWKNPTFFLRVISDTASLCYSILKAKNAGMSLGAKGAAGPLPSEAVQWLCHQAFLL 1080

Qy       1081 KLTRHRVTYVPLLGSLRTAQTQLSRKLPGTTLTALEAAANPALPSDFKTILD 1132

Db       1081 KLTRHRVTYVPLLGSLRTAQTQLSRKLPGTTLTALEAAANPALPSDFKTILD 1132
```

RESULT 5
AAY43621
ID AAY43621 standard; protein; 1132 AA.
XX
AC AAY43621;
XX
DT 26-JAN-2000 (first entry)
XX
DE A human telomerase reverse transcriptase (TRT) polypeptide.
XX
KW Human; telomerase reverse transcriptase; TRT; T lymphocyte activation;
KW dendritic cell; telomerase activity; cancer cell; proliferating cell;
KW immunological destruction; telomerase; cancer; proliferation disease.
XX
OS Homo sapiens.
XX
PN WO9950392-A1.
XX
PD 07-OCT-1999.
XX
PF 30-MAR-1999; 99WO-US006898.
XX
PR 31-MAR-1998; 98US-0112006P.
XX
PA (GERO-) GERON CORP.
XX
PI Gaeta FCA;
XX
DR WPI; 1999-610845/52.
DR N-PSDB; AAZ30154.
XX
PT Eliciting an in vivo immune response for prevention and treatment of
PT cancers.
XX
PS Claim 3; Fig 1; 26pp; English.
XX
CC The present sequence represents a human telomerase reverse transcriptase
CC (TRT) polypeptide. The protein is used in the method of the invention.
CC The specification describes a method for activating a T lymphocyte,
CC comprising contacting the T lymphocyte with a dendritic cell that
CC expresses a TRT peptide in the context of a MHC class I or MHC class II
CC molecule. The protein causes induction of an in vivo immunological
CC response to telomerase activity. Cancer cells are characterized by
CC expression of endogenous TRT gene and the presence of detectable
CC telomerase activity. Therefore, by eliciting a specific immune response
CC to TRT or to TRT-expressing cells, it is possible to selectively target
CC proliferating cells for immunological destruction. The method is used for
CC eliciting an in vivo immune response to telomerase by activating a T
CC lymphocyte, and is useful for prevention and treatment of cancers and
CC other proliferation diseases/conditions
XX
SQ Sequence 1132 AA;

Query Match 100.0%; Score 5961; DB 2; Length 1132;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1132; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```
Qy          1 MPRAPRCRAVRSLLRSHYREVLPLATFVRRLGPQGWRLVQRGDPAAFRALVAQCLVCVPW 60

Db          1 MPRAPRCRAVRSLLRSHYREVLPLATFVRRLGPQGWRLVQRGDPAAFRALVAQCLVCVPW 60

Qy         61 DARPPPAAPSFRQVSCLKELVARVLQRLCERGAKNVLAFGFALLDGARGGPPEAFTTSVR 120

Db         61 DARPPPAAPSFRQVSCLKELVARVLQRLCERGAKNVLAFGFALLDGARGGPPEAFTTSVR 120

Qy        121 SYLPNTVTDALRGSGAWGLLLRRVGDDVLVHLLARCALFVLVAPSCAYQVCGPPLYQLGA 180

Db        121 SYLPNTVTDALRGSGAWGLLLRRVGDDVLVHLLARCALFVLVAPSCAYQVCGPPLYQLGA 180

Qy        181 ATQARPPPHASGPRRRLGCERAWNHSVREAGVPLGLPAPGARRRGGSASRSLPLPKRPRR 240
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                 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 ATQARPPPHASGPRRRLGCERAWNHSVREAGVPLGLPAPGARRRGGSASRSLPLPKRPRR 240

Qy        241 GAAPEPERTPVGQGSWAHPGRTRGPSDRGFCVVSPARPAEEATSLEGALSGTRHSHPSVG 300
                 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 GAAPEPERTPVGQGSWAHPGRTRGPSDRGFCVVSPARPAEEATSLEGALSGTRHSHPSVG 300

Qy        301 RQHHAGPPSTSRPPRPWDTPCPPVYAETKHFLYSSGDKEQLRPSFLLSSLRPSLTGARRL 360
                 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 RQHHAGPPSTSRPPRPWDTPCPPVYAETKHFLYSSGDKEQLRPSFLLSSLRPSLTGARRL 360

Qy        361 VETIFLGSRPWMPGTPRRLPRLPQRYWQMRPLFLELLGNHAQCPYGVLLKTHCPLRAAVT 420
                 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        361 VETIFLGSRPWMPGTPRRLPRLPQRYWQMRPLFLELLGNHAQCPYGVLLKTHCPLRAAVT 420

Qy        421 PAAGVCAREKPQGSVAAPEEEDTDPRRLVQLLRQHSSPWQVYGFVRACLRRLVPPGLWGS 480
                 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        421 PAAGVCAREKPQGSVAAPEEEDTDPRRLVQLLRQHSSPWQVYGFVRACLRRLVPPGLWGS 480

Qy        481 RHNERRFLRNTKKFISLGKHAKLSLQELTWKMSVRDCAWLRRSPGVGCVPAAEHRLREEI 540
                 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        481 RHNERRFLRNTKKFISLGKHAKLSLQELTWKMSVRDCAWLRRSPGVGCVPAAEHRLREEI 540

Qy        541 LAKFLHWLMSVYVVELLRSFFYVTETTFQKNRLFFYRKSVWSKLQSIGIRQHLKRVQLRE 600
                 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        541 LAKFLHWLMSVYVVELLRSFFYVTETTFQKNRLFFYRKSVWSKLQSIGIRQHLKRVQLRE 600

Qy        601 LSEAEVRQHREARPALLTSRLRFIPKPDGLRPIVNMDYVVGARTFRREKRAERLTSRVKA 660
                 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        601 LSEAEVRQHREARPALLTSRLRFIPKPDGLRPIVNMDYVVGARTFRREKRAERLTSRVKA 660

Qy        661 LFSVLNYERARRPGLLGASVLGLDDIHRAWRTFVLRVRAQDPPPELYFVKVDVTGAYDTI 720
                 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        661 LFSVLNYERARRPGLLGASVLGLDDIHRAWRTFVLRVRAQDPPPELYFVKVDVTGAYDTI 720

Qy        721 PQDRLTEVIASIIKPQNTYCVRRYAVVQKAAHGHVRKAFKSHVSTLTDLQPYMRQFVAHL 780
                 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        721 PQDRLTEVIASIIKPQNTYCVRRYAVVQKAAHGHVRKAFKSHVSTLTDLQPYMRQFVAHL 780

Qy        781 QETSPLRDAVVIEQSSSLNEASSGLFDVFLRFMCHHAVRIRGKSYVQCQGIPQGSILSTL 840
                 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        781 QETSPLRDAVVIEQSSSLNEASSGLFDVFLRFMCHHAVRIRGKSYVQCQGIPQGSILSTL 840

Qy        841 LCSLCYGDMENKLFAGIRRDGLLLRLVDDFLLVTPHLTHAKTFLRTLVRGVPEYGCVVNL 900
                 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        841 LCSLCYGDMENKLFAGIRRDGLLLRLVDDFLLVTPHLTHAKTFLRTLVRGVPEYGCVVNL 900

Qy        901 RKTVVNFPVEDEALGGTAFVQMPAHGLFPWCGLLLDTRTLEVQSDYSSYARTSIRASLTF 960
                 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        901 RKTVVNFPVEDEALGGTAFVQMPAHGLFPWCGLLLDTRTLEVQSDYSSYARTSIRASLTF 960

Qy        961 NRGFKAGRNMRRKLFGVLRLKCHSLFLDLQVNSLQTVCTNIYKILLLQAYRFHACVLQLP 1020
                 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        961 NRGFKAGRNMRRKLFGVLRLKCHSLFLDLQVNSLQTVCTNIYKILLLQAYRFHACVLQLP 1020

Qy       1021 FHQQVWKNPTFFLRVISDTASLCYSILKAKNAGMSLGAKGAAGPLPSEAVQWLCHQAFLL 1080
                 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1021 FHQQVWKNPTFFLRVISDTASLCYSILKAKNAGMSLGAKGAAGPLPSEAVQWLCHQAFLL 1080

Qy       1081 KLTRHRVTYVPLLGSLRTAQTQLSRKLPGTTLTALEAAANPALPSDFKTILD 1132
                 ||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1081 KLTRHRVTYVPLLGSLRTAQTQLSRKLPGTTLTALEAAANPALPSDFKTILD 1132
```

RESULT 6
AAY26580
ID AAY26580 standard; protein; 1132 AA.
XX
AC AAY26580;
XX
DT 13-SEP-1999 (first entry)
XX
DE Human telomerase reverse transcriptase (hTERT) enzyme.
XX
KW Telomerase reverse transcriptase; TERT; mouse; telomere length assay;
KW immunogen; enzyme; telomerase-mediated DNA replication; human.
XX
OS Homo sapiens.
XX
PN WO9927113-A1.
XX
PD 03-JUN-1999.
XX
PF 25-NOV-1998; 98WO-US025211.
XX
PR 26-NOV-1997; 97US-00979742.
PR 16-MAR-1998; 98US-00042460.
XX
PA (GERO-) GERON CORP.
PA (YESH) UNIV YESHIVA EINSTEIN COLLEGE.
XX
PI Morin GB, Allsopp R, Depinho R, Greenberg R;
XX
DR WPI; 1999-347722/29.
XX
PT Mouse telomerase reverse transcriptase (mTERT) enzyme proteins and
PT nucleic acids.
XX
PS Disclosure; Fig 3; 135pp; English.
XX
CC The invention relates to a mouse telomerase reverse transcriptase (mTERT)
CC enzyme. Compositions containing mTERT can be used in telomere length
CC assays. Isolated mTERT is useful as an immunogen for the production of
CC monoclonal or polyclonal antibodies. The method is useful for assessing
CC the degree of purification and identification of new mTERT species, such
CC as an mTERT allele, homolog or isoform, or to screen for modulators
CC (antagonists and agonists) of telomerase-mediated DNA replication.
CC Antagonists and agonists of mTERT can be used to modify the activity of
CC other telomerase enzymes such as human TERT (hTERT). The present sequence
CC represents a human TERT enzyme
XX
SQ Sequence 1132 AA;

```
  Query Match             100.0%;  Score 5961;  DB 2;  Length 1132;
  Best Local Similarity   100.0%;  Pred. No. 0;
  Matches 1132;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 MPRAPRCRAVRSLLRSHYREVLPLATFVRRLGPQGWRLVQRGDPAAFRALVAQCLVCVPW 60
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 MPRAPRCRAVRSLLRSHYREVLPLATFVRRLGPQGWRLVQRGDPAAFRALVAQCLVCVPW 60

Qy         61 DARPPPAAPSFRQVSCLKELVARVLQRLCERGAKNVLAFGFALLDGARGGPPEAFTTSVR 120
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 DARPPPAAPSFRQVSCLKELVARVLQRLCERGAKNVLAFGFALLDGARGGPPEAFTTSVR 120

Qy        121 SYLPNTVTDALRGSGAWGLLLRRVGDDVLVHLLARCALFVLVAPSCAYQVCGPPLYQLGA 180
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 SYLPNTVTDALRGSGAWGLLLRRVGDDVLVHLLARCALFVLVAPSCAYQVCGPPLYQLGA 180

Qy        181 ATQARPPPHASGPRRRLGCERAWNHSVREAGVPLGLPAPGARRRGGSASRSLPLPKRPRR 240
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 ATQARPPPHASGPRRRLGCERAWNHSVREAGVPLGLPAPGARRRGGSASRSLPLPKRPRR 240

Qy        241 GAAPEPERTPVGQGSWAHPGRTRGPSDRGFCVVSPARPAEEATSLEGALSGTRHSHPSVG 300
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 GAAPEPERTPVGQGSWAHPGRTRGPSDRGFCVVSPARPAEEATSLEGALSGTRHSHPSVG 300

Qy        301 RQHHAGPPSTSRPPRPWDTPCPPVYAETKHFLYSSGDKEQLRPSFLLSSLRPSLTGARRL 360
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 RQHHAGPPSTSRPPRPWDTPCPPVYAETKHFLYSSGDKEQLRPSFLLSSLRPSLTGARRL 360

Qy        361 VETIFLGSRPWMPGTPRRLPRLPQRYWQMRPLFLELLGNHAQCPYGVLLKTHCPLRAAVT 420
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        361 VETIFLGSRPWMPGTPRRLPRLPQRYWQMRPLFLELLGNHAQCPYGVLLKTHCPLRAAVT 420

Qy        421 PAAGVCAREKPQGSVAAPEEEDTDPRRLVQLLRQHSSPWQVYGFVRACLRRLVPPGLWGS 480
```

```
Db        421 PAAGVCAREKPQGSVAAPEEEDTDPRRLVQLLRQHSSPWQVYGFVRACLRRLVPPGLWGS 480

Qy        481 RHNERRFLRNTKKFISLGKHAKLSLQELTWKMSVRDCAWLRRSPGVGCVPAAEHRLREEI 540
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        481 RHNERRFLRNTKKFISLGKHAKLSLQELTWKMSVRDCAWLRRSPGVGCVPAAEHRLREEI 540

Qy        541 LAKFLHWLMSVYVVELLRSFFYVTETTFQKNRLFFYRKSVWSKLQSIGIRQHLKRVQLRE 600
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        541 LAKFLHWLMSVYVVELLRSFFYVTETTFQKNRLFFYRKSVWSKLQSIGIRQHLKRVQLRE 600

Qy        601 LSEAEVRQHREARPALLTSRLRFIPKPDGLRPIVNMDYVVGARTFRREKRAERLTSRVKA 660
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        601 LSEAEVRQHREARPALLTSRLRFIPKPDGLRPIVNMDYVVGARTFRREKRAERLTSRVKA 660

Qy        661 LFSVLNYERARRPGLLGASVLGLDDIHRAWRTFVLRVRAQDPPPELYFVKVDVTGAYDTI 720
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        661 LFSVLNYERARRPGLLGASVLGLDDIHRAWRTFVLRVRAQDPPPELYFVKVDVTGAYDTI 720

Qy        721 PQDRLTEVIASIIKPQNTYCVRRYAVVQKAAHGHVRKAFKSHVSTLTDLQPYMRQFVAHL 780
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        721 PQDRLTEVIASIIKPQNTYCVRRYAVVQKAAHGHVRKAFKSHVSTLTDLQPYMRQFVAHL 780

Qy        781 QETSPLRDAVVIEQSSSLNEASSGLFDVFLRFMCHHAVRIRGKSYVQCQGIPQGSILSTL 840
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        781 QETSPLRDAVVIEQSSSLNEASSGLFDVFLRFMCHHAVRIRGKSYVQCQGIPQGSILSTL 840

Qy        841 LCSLCYGDMENKLFAGIRRDGLLLRLVDDFLLVTPHLTHAKTFLRTLVRGVPEYGCVVNL 900
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        841 LCSLCYGDMENKLFAGIRRDGLLLRLVDDFLLVTPHLTHAKTFLRTLVRGVPEYGCVVNL 900

Qy        901 RKTVVNFPVEDEALGGTAFVQMPAHGLFPWCGLLLDTRTLEVQSDYSSYARTSIRASLTF 960
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        901 RKTVVNFPVEDEALGGTAFVQMPAHGLFPWCGLLLDTRTLEVQSDYSSYARTSIRASLTF 960

Qy        961 NRGFKAGRNMRRKLFGVLRLKCHSLFLDLQVNSLQTVCTNIYKILLLQAYRFHACVLQLP 1020
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        961 NRGFKAGRNMRRKLFGVLRLKCHSLFLDLQVNSLQTVCTNIYKILLLQAYRFHACVLQLP 1020

Qy       1021 FHQQVWKNPTFFLRVISDTASLCYSILKAKNAGMSLGAKGAAGPLPSEAVQWLCHQAFLL 1080
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1021 FHQQVWKNPTFFLRVISDTASLCYSILKAKNAGMSLGAKGAAGPLPSEAVQWLCHQAFLL 1080

Qy       1081 KLTRHRVTYVPLLGSLRTAQTQLSRKLPGTTLTALEAAANPALPSDFKTILD 1132
              ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1081 KLTRHRVTYVPLLGSLRTAQTQLSRKLPGTTLTALEAAANPALPSDFKTILD 1132


RESULT 7
AAG64859
ID   AAG64859 standard; protein; 1132 AA.
XX
AC   AAG64859;
XX
DT   21-SEP-2001  (first entry)
XX
DE   Heart muscle cell differentiation related protein SEQ ID NO: 31.
XX
KW   Heart muscle cell; human; cell differentiation; heart disease.
XX
OS   Homo sapiens.
XX
PN   WO200148151-A1.
XX
PD   05-JUL-2001.
XX
PF   27-DEC-2000; 2000WO-JP009323.
XX
PR   28-DEC-1999;   99JP-00372826.
PR   28-FEB-2000; 2000WO-JP001148.
PR   02-NOV-2000; 2000WO-JP007741.
XX
PA   (KYOW ) KYOWA HAKKO KOGYO KK.
XX
PI   Umezawa A,  Hata J,  Fukuda K,  Ogawa S,  Sakurada K,  Gojo S;
PI   Yamada Y;
XX
DR   WPI; 2001-425656/45.
DR   N-PSDB; AAH48235.
XX
PT   Cells capable of differentiating into cardiomyocytes and originating in
PT   bone marrow or umbilical blood cells for study of cardiomyocyte
PT   differentiation and treatment of heart disease.
XX
PS   Claim 87; Page 143-147; 183pp; Japanese.
XX
CC   The present invention provides cells originating in the human bone marrow
CC   or umbilical blood cells which are capable of differentiating into
CC   cardiomyocytes. These cells are useful in the treatment of diseases
CC   involving heart muscle degeneration, such as myocardial infarction, and
CC   the study of cardiomyocyte differentiation. The present sequence is a
CC   protein described in the exemplification of the invention
XX
SQ   Sequence 1132 AA;

  Query Match             100.0%;  Score 5961;  DB 4;  Length 1132;
  Best Local Similarity   100.0%;  Pred. No. 0;
  Matches 1132;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 MPRAPRCRAVRSLLRSHYREVLPLATFVRRLGPQGWRLVQRGDPAAFRALVAQCLVCVPW 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 MPRAPRCRAVRSLLRSHYREVLPLATFVRRLGPQGWRLVQRGDPAAFRALVAQCLVCVPW 60

Qy         61 DARPPPAAPSFRQVSCLKELVARVLQRLCERGAKNVLAFGFALLDGARGGPPEAFTTSVR 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 DARPPPAAPSFRQVSCLKELVARVLQRLCERGAKNVLAFGFALLDGARGGPPEAFTTSVR 120

Qy        121 SYLPNTVTDALRGSGAWGLLLRRVGDDVLVHLLARCALFVLVAPSCAYQVCGPPLYQLGA 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 SYLPNTVTDALRGSGAWGLLLRRVGDDVLVHLLARCALFVLVAPSCAYQVCGPPLYQLGA 180

Qy        181 ATQARPPPHASGPRRRLGCERAWNHSVREAGVPLGLPAPGARRRGGSASRSLPLPKRPRR 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 ATQARPPPHASGPRRRLGCERAWNHSVREAGVPLGLPAPGARRRGGSASRSLPLPKRPRR 240

Qy        241 GAAPEPERTPVGQGSWAHPGRTRGPSDRGFCVVSPARPAEEATSLEGALSGTRHSHPSVG 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 GAAPEPERTPVGQGSWAHPGRTRGPSDRGFCVVSPARPAEEATSLEGALSGTRHSHPSVG 300

Qy        301 RQHHAGPPSTSRPPRPWDTPCPPVYAETKHFLYSSGDKEQLRPSFLLSSLRPSLTGARRL 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 RQHHAGPPSTSRPPRPWDTPCPPVYAETKHFLYSSGDKEQLRPSFLLSSLRPSLTGARRL 360

Qy        361 VETIFLGSRPWMPGTPRRLPRLPQRYWQMRPLFLELLGNHAQCPYGVLLKTHCPLRAAVT 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        361 VETIFLGSRPWMPGTPRRLPRLPQRYWQMRPLFLELLGNHAQCPYGVLLKTHCPLRAAVT 420

Qy        421 PAAGVCAREKPQGSVAAPEEEDTDPRRLVQLLRQHSSPWQVYGFVRACLRRLVPPGLWGS 480
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        421 PAAGVCAREKPQGSVAAPEEEDTDPRRLVQLLRQHSSPWQVYGFVRACLRRLVPPGLWGS 480

Qy        481 RHNERRFLRNTKKFISLGKHAKLSLQELTWKMSVRDCAWLRRSPGVGCVPAAEHRLREEI 540
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        481 RHNERRFLRNTKKFISLGKHAKLSLQELTWKMSVRDCAWLRRSPGVGCVPAAEHRLREEI 540

Qy        541 LAKFLHWLMSVYVVELLRSFFYVTETTFQKNRLFFYRKSVWSKLQSIGIRQHLKRVQLRE 600
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        541 LAKFLHWLMSVYVVELLRSFFYVTETTFQKNRLFFYRKSVWSKLQSIGIRQHLKRVQLRE 600

Qy        601 LSEAEVRQHREARPALLTSRLRFIPKPDGLRPIVNMDYVVGARTFRREKRAERLTSRVKA 660
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        601 LSEAEVRQHREARPALLTSRLRFIPKPDGLRPIVNMDYVVGARTFRREKRAERLTSRVKA 660

Qy        661 LFSVLNYERARRPGLLGASVLGLDDIHRAWRTFVLRVRAQDPPPELYFVKVDVTGAYDTI 720
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        661 LFSVLNYERARRPGLLGASVLGLDDIHRAWRTFVLRVRAQDPPPELYFVKVDVTGAYDTI 720
```

```
Qy        721 PQDRLTEVIASIIKPQNTYCVRRYAVVQKAAHGHVRKAFKSHVSTLTDLQPYMRQFVAHL 780
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        721 PQDRLTEVIASIIKPQNTYCVRRYAVVQKAAHGHVRKAFKSHVSTLTDLQPYMRQFVAHL 780

Qy        781 QETSPLRDAVVIEQSSSLNEASSGLFDVFLRFMCHHAVRIRGKSYVQCQGIPQGSILSTL 840
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        781 QETSPLRDAVVIEQSSSLNEASSGLFDVFLRFMCHHAVRIRGKSYVQCQGIPQGSILSTL 840

Qy        841 LCSLCYGDMENKLFAGIRRDGLLLRLVDDFLLVTPHLTHAKTFLRTLVRGVPEYGCVVNL 900
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        841 LCSLCYGDMENKLFAGIRRDGLLLRLVDDFLLVTPHLTHAKTFLRTLVRGVPEYGCVVNL 900

Qy        901 RKTVVNFPVEDEALGGTAFVQMPAHGLFPWCGLLLDTRTLEVQSDYSSYARTSIRASLTF 960
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        901 RKTVVNFPVEDEALGGTAFVQMPAHGLFPWCGLLLDTRTLEVQSDYSSYARTSIRASLTF 960

Qy        961 NRGFKAGRNMRRKLFGVLRLKCHSLFLDLQVNSLQTVCTNIYKILLLQAYRFHACVLQLP 1020
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        961 NRGFKAGRNMRRKLFGVLRLKCHSLFLDLQVNSLQTVCTNIYKILLLQAYRFHACVLQLP 1020

Qy       1021 FHQQVWKNPTFFLRVISDTASLCYSILKAKNAGMSLGAKGAAGPLPSEAVQWLCHQAFLL 1080
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1021 FHQQVWKNPTFFLRVISDTASLCYSILKAKNAGMSLGAKGAAGPLPSEAVQWLCHQAFLL 1080

Qy       1081 KLTRHRVTYVPLLGSLRTAQTQLSRKLPGTTLTALEAAANPALPSDFKTILD 1132
              ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1081 KLTRHRVTYVPLLGSLRTAQTQLSRKLPGTTLTALEAAANPALPSDFKTILD 1132
```

RESULT 8
AAG64329
ID AAG64329 standard; protein; 1132 AA.
XX
AC AAG64329;
XX
DT 24-SEP-2001 (first entry)
XX
DE Human protein #2.
XX
KW Angiogenesis; cardiant; cell differentiating agent; bone marrow;
KW heart muscle cell; heart disease; human.
XX
OS Homo sapiens.
XX
PN WO200148149-A1.
XX
PD 05-JUL-2001.
XX
PF 28-FEB-2000; 2000WO-JP001148.
XX
PR 28-DEC-1999; 99JP-00372826.
XX
PA (KYOW) KYOWA HAKKO KOGYO KK.
XX
PI Umezawa A, Hata J, Fukuda K, Ogawa S, Sakurada K;
XX
DR WPI; 2001-418252/44.
DR N-PSDB; AAH49601.
XX
PT New adult bone marrow-originated cells capable of differentiating into
PT heart muscle cells, applicable as remedies for various heart diseases
PT particularly with damaged heart muscle accompanying degeneration.
XX
PS Disclosure; Page 128-134; 158pp; Japanese.
XX
CC The present invention relates to cells isolated from bone marrow, which
CC are capable of at least differentiating into heart muscle cells. The
CC cells are applicable as remedies for various heart diseases particularly
CC with damaged heart muscle accompanying degeneration. The present sequence
CC was used to illustrate the present invention
XX
SQ Sequence 1132 AA;

```
  Query Match           100.0%;  Score 5961;  DB 4;  Length 1132;
  Best Local Similarity  100.0%;  Pred. No. 0;
  Matches 1132;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 MPRAPRCRAVRSLLRSHYREVLPLATFVRRLGPQGWRLVQRGDPAAFRALVAQCLVCVPW 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 MPRAPRCRAVRSLLRSHYREVLPLATFVRRLGPQGWRLVQRGDPAAFRALVAQCLVCVPW 60

Qy         61 DARPPPAAPSFRQVSCLKELVARVLQRLCERGAKNVLAFGFALLDGARGGPPEAFTTSVR 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 DARPPPAAPSFRQVSCLKELVARVLQRLCERGAKNVLAFGFALLDGARGGPPEAFTTSVR 120

Qy        121 SYLPNTVTDALRGSGAWGLLLRRVGDDVLVHLLARCALFVLVAPSCAYQVCGPPLYQLGA 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 SYLPNTVTDALRGSGAWGLLLRRVGDDVLVHLLARCALFVLVAPSCAYQVCGPPLYQLGA 180

Qy        181 ATQARPPPHASGPRRRLGCERAWNHSVREAGVPLGLPAPGARRRGGSASRSLPLPKRPRR 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 ATQARPPPHASGPRRRLGCERAWNHSVREAGVPLGLPAPGARRRGGSASRSLPLPKRPRR 240

Qy        241 GAAPEPERTPVGQGSWAHPGRTRGPSDRGFCVVSPARPAEEATSLEGALSGTRHSHPSVG 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 GAAPEPERTPVGQGSWAHPGRTRGPSDRGFCVVSPARPAEEATSLEGALSGTRHSHPSVG 300

Qy        301 RQHHAGPPSTSRPPRPWDTPCPPVYAETKHFLYSSGDKEQLRPSFLLSSLRPSLTGARRL 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 RQHHAGPPSTSRPPRPWDTPCPPVYAETKHFLYSSGDKEQLRPSFLLSSLRPSLTGARRL 360

Qy        361 VETIFLGSRPWMPGTPRRLPRLPQRYWQMRPLFLELLGNHAQCPYGVLLKTHCPLRAAVT 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        361 VETIFLGSRPWMPGTPRRLPRLPQRYWQMRPLFLELLGNHAQCPYGVLLKTHCPLRAAVT 420

Qy        421 PAAGVCAREKPQGSVAAPEEEDTDPRRLVQLLRQHSSPWQVYGFVRACLRRLVPPGLWGS 480
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        421 PAAGVCAREKPQGSVAAPEEEDTDPRRLVQLLRQHSSPWQVYGFVRACLRRLVPPGLWGS 480

Qy        481 RHNERRFLRNTKKFISLGKHAKLSLQELTWKMSVRDCAWLRRSPGVGCVPAAEHRLREEI 540
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        481 RHNERRFLRNTKKFISLGKHAKLSLQELTWKMSVRDCAWLRRSPGVGCVPAAEHRLREEI 540

Qy        541 LAKFLHWLMSVYVVELLRSFFYVTETTFQKNRLFFYRKSVWSKLQSIGIRQHLKRVQLRE 600
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        541 LAKFLHWLMSVYVVELLRSFFYVTETTFQKNRLFFYRKSVWSKLQSIGIRQHLKRVQLRE 600

Qy        601 LSEAEVRQHREARPALLTSRLRFIPKPDGLRPIVNMDYVVGARTFRREKRAERLTSRVKA 660
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        601 LSEAEVRQHREARPALLTSRLRFIPKPDGLRPIVNMDYVVGARTFRREKRAERLTSRVKA 660

Qy        661 LFSVLNYERARRPGLLGASVLGLDDIHRAWRTFVLRVRAQDPPPELYFVKVDVTGAYDTI 720
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        661 LFSVLNYERARRPGLLGASVLGLDDIHRAWRTFVLRVRAQDPPPELYFVKVDVTGAYDTI 720

Qy        721 PQDRLTEVIASIIKPQNTYCVRRYAVVQKAAHGHVRKAFKSHVSTLTDLQPYMRQFVAHL 780
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        721 PQDRLTEVIASIIKPQNTYCVRRYAVVQKAAHGHVRKAFKSHVSTLTDLQPYMRQFVAHL 780

Qy        781 QETSPLRDAVVIEQSSSLNEASSGLFDVFLRFMCHHAVRIRGKSYVQCQGIPQGSILSTL 840
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        781 QETSPLRDAVVIEQSSSLNEASSGLFDVFLRFMCHHAVRIRGKSYVQCQGIPQGSILSTL 840

Qy        841 LCSLCYGDMENKLFAGIRRDGLLLRLVDDFLLVTPHLTHAKTFLRTLVRGVPEYGCVVNL 900
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        841 LCSLCYGDMENKLFAGIRRDGLLLRLVDDFLLVTPHLTHAKTFLRTLVRGVPEYGCVVNL 900

Qy        901 RKTVVNFPVEDEALGGTAFVQMPAHGLFPWCGLLLDTRTLEVQSDYSSYARTSIRASLTF 960
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        901 RKTVVNFPVEDEALGGTAFVQMPAHGLFPWCGLLLDTRTLEVQSDYSSYARTSIRASLTF 960

Qy        961 NRGFKAGRNMRRKLFGVLRLKCHSLFLDLQVNSLQTVCTNIYKILLLQAYRFHACVLQLP 1020
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        961 NRGFKAGRNMRRKLFGVLRLKCHSLFLDLQVNSLQTVCTNIYKILLLQAYRFHACVLQLP 1020
```

```
Qy       1021 FHQQVWKNPTFFLRVISDTASLCYSILKAKNAGMSLGAKGAAGPLPSEAVQWLCHQAFLL 1080
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1021 FHQQVWKNPTFFLRVISDTASLCYSILKAKNAGMSLGAKGAAGPLPSEAVQWLCHQAFLL 1080

Qy       1081 KLTRHRVTYVPLLGSLRTAQTQLSRKLPGTTLTALEAAANPALPSDFKTILD 1132
             |||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1081 KLTRHRVTYVPLLGSLRTAQTQLSRKLPGTTLTALEAAANPALPSDFKTILD 1132


RESULT 9
AAB99930
ID   AAB99930 standard; protein; 1132 AA.
XX
AC   AAB99930;
XX
DT   26-SEP-2001  (first entry)
XX
DE   Human telomerase protein sequence SEQ ID NO:31.
XX
KW   Differentiation; heart muscle cell; cytokine; transcription factor;
KW   proliferation; surface antigen; heart disease; cardiomyocyte;
KW   bone marrow; umbilical blood cell; heart muscle degeneration;
KW   myocardial infarction.
XX
OS   Homo sapiens.
XX
PN   WO200148150-A1.
XX
PD   05-JUL-2001.
XX
PF   02-NOV-2000; 2000WO-JP007741.
XX
PR   28-DEC-1999;   99JP-00372826.
PR   28-FEB-2000; 2000WO-JP001148.
XX
PA   (KYOW ) KYOWA HAKKO KOGYO KK.
XX
PI   Umezawa A,  Hata J,  Fukuda K,  Ogawa S,  Sakurada K,  Gojo S;
PI   Yamada Y;
XX
DR   WPI; 2001-425655/45.
DR   N-PSDB; AAH44366.
XX
PT   Cells capable of differentiating into cardiomyocytes and originating in
PT   bone marrow or umbilical blood cells for study of cardiomyocyte
PT   differentiation and treatment of heart disease.
XX
PS   Claim 146; Page 137-141; 187pp; Japanese.
XX
CC   The present invention describes cells originating in bone marrow or
CC   umbilical blood cells which are capable of differentiating into
CC   cardiomyocytes. Also described are: (1) cardiomyocytes produced by the
CC   differentiation of the cells; (2) a method for carrying out the
CC   differentiation into cardiomyocytes, regulated by a promotional and/or
CC   inhibitory factor; (3) a method for the differentiation of the cells into
CC   cell types other than cardiomyocytes; (4) drug compositions promoting the
CC   formation of heart muscle and regeneration of heart tissue which contain
CC   the cells; (5) a method for the production of antibodies which recognise
CC   the cells, especially antibodies which recognise a surface antigen on the
CC   cells; (6) a method for screening factors which promote the proliferation
CC   of the cells; (7) a method for immortalising the cells by expressing
CC   telomerase in them; (8) drug compositions for the treatment of heart
CC   disease which contain the immortalised cells; and (9) cell-free
CC   supernatant from the culture of the cells and its use in promoting their
CC   differentiation into cardiomyocytes. The cells are used in the treatment
CC   of diseases involving heart muscle degeneration, such as myocardial
CC   infarction and in the study of cardiomyocyte differentiation. AAH44351 to
CC   AAH44409 and AAB99915 to AAB99935 represent sequences used in the
CC   exemplification of the present invention
XX
SQ   Sequence 1132 AA;

  Query Match             100.0%;  Score 5961;  DB 4;  Length 1132;
  Best Local Similarity   100.0%;  Pred. No. 0;
  Matches 1132;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 MPRAPRCRAVRSLLRSHYREVLPLATFVRRLGPQGWRLVQRGDPAAFRALVAQCLVCVPW 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 MPRAPRCRAVRSLLRSHYREVLPLATFVRRLGPQGWRLVQRGDPAAFRALVAQCLVCVPW 60

Qy         61 DARPPPAAPSFRQVSCLKELVARVLQRLCERGAKNVLAFGFALLDGARGGPPEAFTTSVR 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 DARPPPAAPSFRQVSCLKELVARVLQRLCERGAKNVLAFGFALLDGARGGPPEAFTTSVR 120

Qy        121 SYLPNTVTDALRGSGAWGLLLRRVGDDVLVHLLARCALFVLVAPSCAYQVCGPPLYQLGA 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 SYLPNTVTDALRGSGAWGLLLRRVGDDVLVHLLARCALFVLVAPSCAYQVCGPPLYQLGA 180

Qy        181 ATQARPPPHASGPRRRLGCERAWNHSVREAGVPLGLPAPGARRRGGSASRSLPLPKRPRR 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 ATQARPPPHASGPRRRLGCERAWNHSVREAGVPLGLPAPGARRRGGSASRSLPLPKRPRR 240

Qy        241 GAAPEPERTPVGQGSWAHPGRTRGPSDRGFCVVSPARPAEEATSLEGALSGTRHSHPSVG 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 GAAPEPERTPVGQGSWAHPGRTRGPSDRGFCVVSPARPAEEATSLEGALSGTRHSHPSVG 300

Qy        301 RQHHAGPPSTSRPPRPWDTPCPPVYAETKHFLYSSGDKEQLRPSFLLSSLRPSLTGARRL 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 RQHHAGPPSTSRPPRPWDTPCPPVYAETKHFLYSSGDKEQLRPSFLLSSLRPSLTGARRL 360

Qy        361 VETIFLGSRPWMPGTPRRLPRLPQRYWQMRPLFLELLGNHAQCPYGVLLKTHCPLRAAVT 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        361 VETIFLGSRPWMPGTPRRLPRLPQRYWQMRPLFLELLGNHAQCPYGVLLKTHCPLRAAVT 420

Qy        421 PAAGVCAREKPQGSVAAPEEEDTDPRRLVQLLRQHSSPWQVYGFVRACLRRLVPPGLWGS 480
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        421 PAAGVCAREKPQGSVAAPEEEDTDPRRLVQLLRQHSSPWQVYGFVRACLRRLVPPGLWGS 480

Qy        481 RHNERRFLRNTKKFISLGKHAKLSLQELTWKMSVRDCAWLRRSPGVGCVPAAEHRLREEI 540
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        481 RHNERRFLRNTKKFISLGKHAKLSLQELTWKMSVRDCAWLRRSPGVGCVPAAEHRLREEI 540

Qy        541 LAKFLHWLMSVYVVELLRSFFYVTETTFQKNRLFFYRKSVWSKLQSIGIRQHLKRVQLRE 600
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        541 LAKFLHWLMSVYVVELLRSFFYVTETTFQKNRLFFYRKSVWSKLQSIGIRQHLKRVQLRE 600

Qy        601 LSEAEVRQHREARPALLTSRLRFIPKPDGLRPIVNMDYVVGARTFRREKRAERLTSRVKA 660
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        601 LSEAEVRQHREARPALLTSRLRFIPKPDGLRPIVNMDYVVGARTFRREKRAERLTSRVKA 660

Qy        661 LFSVLNYERARRPGLLGASVLGLDDIHRAWRTFVLRVRAQDPPPELYFVKVDVTGAYDTI 720
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        661 LFSVLNYERARRPGLLGASVLGLDDIHRAWRTFVLRVRAQDPPPELYFVKVDVTGAYDTI 720

Qy        721 PQDRLTEVIASIIKPQNTYCVRRYAVVQKAAHGHVRKAFKSHVSTLTDLQPYMRQFVAHL 780
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        721 PQDRLTEVIASIIKPQNTYCVRRYAVVQKAAHGHVRKAFKSHVSTLTDLQPYMRQFVAHL 780

Qy        781 QETSPLRDAVVIEQSSSLNEASSGLFDVFLRFMCHHAVRIRGKSYVQCQGIPQGSILSTL 840
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        781 QETSPLRDAVVIEQSSSLNEASSGLFDVFLRFMCHHAVRIRGKSYVQCQGIPQGSILSTL 840

Qy        841 LCSLCYGDMENKLFAGIRRDGLLLRLVDDFLLVTPHLTHAKTFLRTLVRGVPEYGCVVNL 900
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        841 LCSLCYGDMENKLFAGIRRDGLLLRLVDDFLLVTPHLTHAKTFLRTLVRGVPEYGCVVNL 900

Qy        901 RKTVVNFPVEDEALGGTAFVQMPAHGLFPWCGLLLDTRTLEVQSDYSSYARTSIRASLTF 960
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        901 RKTVVNFPVEDEALGGTAFVQMPAHGLFPWCGLLLDTRTLEVQSDYSSYARTSIRASLTF 960

Qy        961 NRGFKAGRNMRRKLFGVLRLKCHSLFLDLQVNSLQTVCTNIYKILLLQAYRFHACVLQLP 1020
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        961 NRGFKAGRNMRRKLFGVLRLKCHSLFLDLQVNSLQTVCTNIYKILLLQAYRFHACVLQLP 1020

Qy       1021 FHQQVWKNPTFFLRVISDTASLCYSILKAKNAGMSLGAKGAAGPLPSEAVQWLCHQAFLL 1080
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
```

```
Db       1021 FHQQVWKNPTFFLRVISDTASLCYSILKAKNAGMSLGAKGAAGPLPSEAVQWLCHQAFLL 1080

Qy       1081 KLTRHRVTYVPLLGSLRTAQTQLSRKLPGTTLTALEAAANPALPSDFKTILD 1132
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1081 KLTRHRVTYVPLLGSLRTAQTQLSRKLPGTTLTALEAAANPALPSDFKTILD 1132


RESULT 10
AAB82765
ID   AAB82765 standard; protein; 1132 AA.
XX
AC   AAB82765;
XX
DT   29-OCT-2001  (first entry)
XX
DE   Human telomerase reverse transcriptase.
XX
KW   Telomerase reverse transcriptase; hTRT; human; cancer; tumour;
KW   cytotoxic T lymphocyte; major histocompatibility complex;
KW   human leucocyte antigen; HLA-A2.1; vaccine.
XX
OS   Homo sapiens.
XX
FH   Key             Location/Qualifiers
FT   Peptide         13. .21
FT                   /note= "HLA-A2.1 binding motif"
FT   Peptide         23. .31
FT                   /note= "HLA-A2.1 binding motif"
FT   Peptide         76. .84
FT                   /note= "HLA-A2.1 binding motif"
FT   Peptide         96. .104
FT                   /note= "HLA-A2.1 binding motif"
FT   Peptide         140. .148
FT                   /note= "HLA-A2.1 binding motif"
FT   Peptide         152. .160
FT                   /note= "HLA-A2.1 binding motif"
FT   Peptide         346. .354
FT                   /note= "HLA-A2.1 binding motif"
FT   Peptide         353. .361
FT                   /note= "HLA-A2.1 binding motif"
FT   Peptide         371. .379
FT                   /note= "HLA-A2.1 binding motif"
FT   Peptide         388. .396
FT                   /note= "HLA-A2.1 binding motif"
FT   Peptide         407. .415
FT                   /note= "HLA-A2.1 binding motif"
FT   Peptide         487. .495
FT                   /note= "HLA-A2.1 binding motif"
FT   Peptide         540. .548
FT                   /label= p540
FT                   /note= "HLA-A2.1 binding motif"
FT   Peptide         548. .556
FT                   /note= "HLA-A2.1 binding motif"
FT   Peptide         555. .563
FT                   /note= "HLA-A2.1 binding motif"
FT   Peptide         572. .580
FT                   /note= "HLA-A2.1 binding motif"
FT   Peptide         705. .713
FT                   /note= "HLA-A2.1 binding motif"
FT   Peptide         724. .732
FT                   /note= "HLA-A2.1 binding motif"
FT   Peptide         772. .780
FT                   /note= "HLA-A2.1 binding motif"
FT   Peptide         797. .805
FT                   /note= "HLA-A2.1 binding motif"
FT   Peptide         812. .820
FT                   /note= "HLA-A2.1 binding motif"
FT   Peptide         836. .844
FT                   /note= "HLA-A2.1 binding motif"
FT   Peptide         863. .871
FT                   /note= "HLA-A2.1 binding motif"
FT   Peptide         865. .873
FT                   /label= p865
FT                   /note= "HLA-A2.1 binding motif"
FT   Peptide         883. .891
FT                   /note= "HLA-A2.1 binding motif"
FT   Peptide         926. .934
FT                   /note= "HLA-A2.1 binding motif"
FT   Peptide         934. .942
FT                   /note= "HLA-A2.1 binding motif"
FT   Peptide         969. .977
FT                   /note= "HLA-A2.1 binding motif"
FT   Peptide         988. .996
FT                   /note= "HLA-A2.1 binding motif"
FT   Peptide         1072. .1080
FT                   /note= "HLA-A2.1 binding motif"
FT   Peptide         1079. .1087
FT                   /note= "HLA-A2.1 binding motif"
FT   Peptide         1095. .1103
FT                   /note= "HLA-A2.1 binding motif"
FT   Peptide         1122. .1130
FT                   /note= "HLA-A2.1 binding motif"
XX
PN   WO200160391-A1.
XX
PD   23-AUG-2001.
XX
PF   15-FEB-2001; 2001WO-US005143.
XX
PR   15-FEB-2000; 2000US-0182685P.
PR   15-FEB-2001; 2001US-00182685.
XX
PA   (REGC ) UNIV CALIFORNIA.
XX
PI   Zanetti M;
XX
DR   WPI; 2001-536552/59.
XX
PT   Vaccine for initiating and enhancing a cytotoxic T lymphocyte response,
PT   for treating cancers or tumors or for inducing immune response against
PT   tumors, comprises a telomerase reverse transcriptase peptide.
XX
PS   Disclosure; Fig 5; 52pp; English.
XX
CC   The present sequence is that of human telomerase reverse transcriptase
CC   (hTRT). The sequence was analysed for 9-mer peptide sequences containing
CC   known binding motifs for the human leukocyte antigen HLA-A2.1 molecule.
CC   From an initial panel of about 30 candidate peptides, 2 sequences,
CC   denoted p540 (see AAB82772) and p865 (see AAB82773), were examined. The
CC   majority of healthy individuals as well as patients with prostate cancer
CC   immunised in vitro against these 2 HLA-A2.1 restricted peptides developed
CC   hTRT-specific cytotoxic T lymphocytes (CTL). The cancer patients' CTL
CC   specifically lysed a variety of HLA-A2+ cancer cell lines such as
CC   prostate, breast, colon, lung and melanoma, demonstrating immunological
CC   recognition of endogenously-processed hTRT peptides. In vivo immunisation
CC   of HLA-A2.1 transgenic mice generated a specific CTL response against
CC   both hTRT peptides. The induction of CTL responses in vitro and in vivo,
CC   and the susceptibility to lysis of tumour cells of various origins by
CC   hTRT CTL suggest that hTRT could serve as a universal cancer vaccine for
CC   humans. Thus, a claimed universal vaccine for treating tumours of any
CC   origin comprises at least 1 hTRT peptide in an amount effective for
CC   initiating and enhancing a CTL response against cancer cells. The peptide
CC   is 7-15 amino acid residues in length and may be modified to enhance
CC   binding to the major histocompatibility complex. Also claimed is a method
CC   for inducing and enhancing a CTL response against cancer cells, involving
CC   harvesting blood leucocytes, pulsing with hTRT, and contacting cancer
CC   cells with the pulsed leucocytes. A method for targeting CTL to tumour
CC   cells is also claimed, and involves administering a hTRT peptide to a
CC   mammal, especially a cancer patient
XX
SQ   Sequence 1132 AA;

  Query Match             100.0%;  Score 5961;  DB 4;  Length 1132;
  Best Local Similarity   100.0%;  Pred. No. 0;
  Matches 1132;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;
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Qy          1 MPRAPRCRAVRSLLRSHYREVLPLATFVRRLGPQGWRLVQRGDPAAFRALVAQCLVCVPW 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 MPRAPRCRAVRSLLRSHYREVLPLATFVRRLGPQGWRLVQRGDPAAFRALVAQCLVCVPW 60

Qy         61 DARPPPAAPSFRQVSCLKELVARVLQRLCERGAKNVLAFGFALLDGARGGPPEAFTTSVR 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 DARPPPAAPSFRQVSCLKELVARVLQRLCERGAKNVLAFGFALLDGARGGPPEAFTTSVR 120

Qy        121 SYLPNTVTDALRGSGAWGLLLRRVGDDVLVHLLARCALFVLVAPSCAYQVCGPPLYQLGA 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 SYLPNTVTDALRGSGAWGLLLRRVGDDVLVHLLARCALFVLVAPSCAYQVCGPPLYQLGA 180

Qy        181 ATQARPPPHASGPRRRLGCERAWNHSVREAGVPLGLPAPGARRRGGSASRSLPLPKRPRR 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 ATQARPPPHASGPRRRLGCERAWNHSVREAGVPLGLPAPGARRRGGSASRSLPLPKRPRR 240

Qy        241 GAAPEPERTPVGQGSWAHPGRTRGPSDRGFCVVSPARPAEEATSLEGALSGTRHSHPSVG 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 GAAPEPERTPVGQGSWAHPGRTRGPSDRGFCVVSPARPAEEATSLEGALSGTRHSHPSVG 300

Qy        301 RQHHAGPPSTSRPPRPWDTPCPPVYAETKHFLYSSGDKEQLRPSFLLSSLRPSLTGARRL 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 RQHHAGPPSTSRPPRPWDTPCPPVYAETKHFLYSSGDKEQLRPSFLLSSLRPSLTGARRL 360

Qy        361 VETIFLGSRPWMPGTPRRLPRLPQRYWQMRPLFLELLGNHAQCPYGVLLKTHCPLRAAVT 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        361 VETIFLGSRPWMPGTPRRLPRLPQRYWQMRPLFLELLGNHAQCPYGVLLKTHCPLRAAVT 420

Qy        421 PAAGVCAREKPQGSVAAPEEEDTDPRRLVQLLRQHSSPWQVYGFVRACLRRLVPPGLWGS 480
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        421 PAAGVCAREKPQGSVAAPEEEDTDPRRLVQLLRQHSSPWQVYGFVRACLRRLVPPGLWGS 480

Qy        481 RHNERRFLRNTKKFISLGKHAKLSLQELTWKMSVRDCAWLRRSPGVGCVPAAEHRLREEI 540
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        481 RHNERRFLRNTKKFISLGKHAKLSLQELTWKMSVRDCAWLRRSPGVGCVPAAEHRLREEI 540

Qy        541 LAKFLHWLMSVYVVELLRSFFYVTETTFQKNRLFFYRKSVWSKLQSIGIRQHLKRVQLRE 600
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        541 LAKFLHWLMSVYVVELLRSFFYVTETTFQKNRLFFYRKSVWSKLQSIGIRQHLKRVQLRE 600

Qy        601 LSEAEVRQHREARPALLTSRLRFIPKPDGLRPIVNMDYVVGARTFRREKRAERLTSRVKA 660
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        601 LSEAEVRQHREARPALLTSRLRFIPKPDGLRPIVNMDYVVGARTFRREKRAERLTSRVKA 660

Qy        661 LFSVLNYERARRPGLLGASVLGLDDIHRAWRTFVLRVRAQDPPPELYFVKVDVTGAYDTI 720
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        661 LFSVLNYERARRPGLLGASVLGLDDIHRAWRTFVLRVRAQDPPPELYFVKVDVTGAYDTI 720

Qy        721 PQDRLTEVIASIIKPQNTYCVRRYAVVQKAAHGHVRKAFKSHVSTLTDLQPYMRQFVAHL 780
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        721 PQDRLTEVIASIIKPQNTYCVRRYAVVQKAAHGHVRKAFKSHVSTLTDLQPYMRQFVAHL 780

Qy        781 QETSPLRDAVVIEQSSSLNEASSGLFDVFLRFMCHHAVRIRGKSYVQCQGIPQGSILSTL 840
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        781 QETSPLRDAVVIEQSSSLNEASSGLFDVFLRFMCHHAVRIRGKSYVQCQGIPQGSILSTL 840

Qy        841 LCSLCYGDMENKLFAGIRRDGLLLRLVDDFLLVTPHLTHAKTFLRTLVRGVPEYGCVVNL 900
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        841 LCSLCYGDMENKLFAGIRRDGLLLRLVDDFLLVTPHLTHAKTFLRTLVRGVPEYGCVVNL 900

Qy        901 RKTVVNFPVEDEALGGTAFVQMPAHGLFPWCGLLLDTRTLEVQSDYSSYARTSIRASLTF 960
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        901 RKTVVNFPVEDEALGGTAFVQMPAHGLFPWCGLLLDTRTLEVQSDYSSYARTSIRASLTF 960

Qy        961 NRGFKAGRNMRRKLFGVLRLKCHSLFLDLQVNSLQTVCTNIYKILLLQAYRFHACVLQLP 1020
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        961 NRGFKAGRNMRRKLFGVLRLKCHSLFLDLQVNSLQTVCTNIYKILLLQAYRFHACVLQLP 1020

Qy       1021 FHQQVWKNPTFFLRVISDTASLCYSILKAKNAGMSLGAKGAAGPLPSEAVQWLCHQAFLL 1080
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1021 FHQQVWKNPTFFLRVISDTASLCYSILKAKNAGMSLGAKGAAGPLPSEAVQWLCHQAFLL 1080

Qy       1081 KLTRHRVTYVPLLGSLRTAQTQLSRKLPGTTLTALEAAANPALPSDFKTILD 1132
              ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1081 KLTRHRVTYVPLLGSLRTAQTQLSRKLPGTTLTALEAAANPALPSDFKTILD 1132
```

RESULT 11
AAE29226
ID AAE29226 standard; protein; 1132 AA.
XX
AC AAE29226;
XX
DT 27-JAN-2003 (first entry)
XX
DE Human telomerase reverse transcriptase (TERT).
XX
KW Carbohydrate antigen; alpha(1,3)galactosyltransferase; alpha1,3GT; TERT;
KW transgenic; alpha(1,2)fucosyltransferase; alpha1,2FT; human; enzyme;
KW telomerase reverse transcriptase.
XX
OS Homo sapiens.
XX
PN WO200274948-A2.
XX
PD 26-SEP-2002.
XX
PF 21-MAR-2002; 2002WO-CA000378.
XX
PR 21-MAR-2001; 2001US-0277811P.
XX
PA (GERO-) GERON CORP.
XX
PI Denning C, Clark AJ, Schiff JM;
XX
DR WPI; 2002-759895/82.
DR N-PSDB; AAD46821.
XX
PT Mammalian cells, useful for producing animal tissues with carbohydrate
PT antigens that are compatible for transplantation into human patients.
XX
PS Disclosure; Page 34; 71pp; English.
XX
CC The invention relates to animal tissues with carbohydrate antigens that
CC are compatible for transplantation into human patients. The mammalian
CC cell is inactivated homozygously for expression of alpha(1,3)galactosyl-
CC transferase (alpha1,3GT) gene and comprises a transgene for alpha(1,2)-
CC fucosyltransferase (alpha1,2FT). It is useful for producing animal tissue
CC with carbohydrate antigens that are compatible for transplantation into
CC human patients. The present sequence is human telomerase reverse
CC transcriptase (TERT) used in the invention
XX
SQ Sequence 1132 AA;

Query Match 100.0%; Score 5961; DB 5; Length 1132;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1132; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy          1 MPRAPRCRAVRSLLRSHYREVLPLATFVRRLGPQGWRLVQRGDPAAFRALVAQCLVCVPW 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 MPRAPRCRAVRSLLRSHYREVLPLATFVRRLGPQGWRLVQRGDPAAFRALVAQCLVCVPW 60

Qy         61 DARPPPAAPSFRQVSCLKELVARVLQRLCERGAKNVLAFGFALLDGARGGPPEAFTTSVR 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 DARPPPAAPSFRQVSCLKELVARVLQRLCERGAKNVLAFGFALLDGARGGPPEAFTTSVR 120

Qy        121 SYLPNTVTDALRGSGAWGLLLRRVGDDVLVHLLARCALFVLVAPSCAYQVCGPPLYQLGA 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 SYLPNTVTDALRGSGAWGLLLRRVGDDVLVHLLARCALFVLVAPSCAYQVCGPPLYQLGA 180

Qy        181 ATQARPPPHASGPRRRLGCERAWNHSVREAGVPLGLPAPGARRRGGSASRSLPLPKRPRR 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 ATQARPPPHASGPRRRLGCERAWNHSVREAGVPLGLPAPGARRRGGSASRSLPLPKRPRR 240

Qy        241 GAAPEPERTPVGQGSWAHPGRTRGPSDRGFCVVSPARPAEEATSLEGALSGTRHSHPSVG 300
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Db        241 GAAPEPERTPVGQGSWAHPGRTRGPSDRGFCVVSPARPAEEATSLEGALSGTRHSHPSVG 300

Qy        301 RQHHAGPPSTSRPPRPWDTPCPPVYAETKHFLYSSGDKEQLRPSFLLSSLRPSLTGARRL 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 RQHHAGPPSTSRPPRPWDTPCPPVYAETKHFLYSSGDKEQLRPSFLLSSLRPSLTGARRL 360

Qy        361 VETIFLGSRPWMPGTPRRLPRLPQRYWQMRPLFLELLGNHAQCPYGVLLKTHCPLRAAVT 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        361 VETIFLGSRPWMPGTPRRLPRLPQRYWQMRPLFLELLGNHAQCPYGVLLKTHCPLRAAVT 420

Qy        421 PAAGVCAREKPQGSVAAPEEEDTDPRRLVQLLRQHSSPWQVYGFVRACLRRLVPPGLWGS 480
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        421 PAAGVCAREKPQGSVAAPEEEDTDPRRLVQLLRQHSSPWQVYGFVRACLRRLVPPGLWGS 480

Qy        481 RHNERRFLRNTKKFISLGKHAKLSLQELTWKMSVRDCAWLRRSPGVGCVPAAEHRLREEI 540
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        481 RHNERRFLRNTKKFISLGKHAKLSLQELTWKMSVRDCAWLRRSPGVGCVPAAEHRLREEI 540

Qy        541 LAKFLHWLMSVYVVELLRSFFYVTETTFQKNRLFFYRKSVWSKLQSIGIRQHLKRVQLRE 600
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        541 LAKFLHWLMSVYVVELLRSFFYVTETTFQKNRLFFYRKSVWSKLQSIGIRQHLKRVQLRE 600

Qy        601 LSEAEVRQHREARPALLTSRLRFIPKPDGLRPIVNMDYVVGARTFRREKRAERLTSRVKA 660
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        601 LSEAEVRQHREARPALLTSRLRFIPKPDGLRPIVNMDYVVGARTFRREKRAERLTSRVKA 660

Qy        661 LFSVLNYERARRPGLLGASVLGLDDIHRAWRTFVLRVRAQDPPPELYFVKVDVTGAYDTI 720
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        661 LFSVLNYERARRPGLLGASVLGLDDIHRAWRTFVLRVRAQDPPPELYFVKVDVTGAYDTI 720

Qy        721 PQDRLTEVIASIIKPQNTYCVRRYAVVQKAAHGHVRKAFKSHVSTLTDLQPYMRQFVAHL 780
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        721 PQDRLTEVIASIIKPQNTYCVRRYAVVQKAAHGHVRKAFKSHVSTLTDLQPYMRQFVAHL 780

Qy        781 QETSPLRDAVVIEQSSSLNEASSGLFDVFLRFMCHHAVRIRGKSYVQCQGIPQGSILSTL 840
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        781 QETSPLRDAVVIEQSSSLNEASSGLFDVFLRFMCHHAVRIRGKSYVQCQGIPQGSILSTL 840

Qy        841 LCSLCYGDMENKLFAGIRRDGLLLRLVDDFLLVTPHLTHAKTFLRTLVRGVPEYGCVVNL 900
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        841 LCSLCYGDMENKLFAGIRRDGLLLRLVDDFLLVTPHLTHAKTFLRTLVRGVPEYGCVVNL 900

Qy        901 RKTVVNFPVEDEALGGTAFVQMPAHGLFPWCGLLLDTRTLEVQSDYSSYARTSIRASLTF 960
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        901 RKTVVNFPVEDEALGGTAFVQMPAHGLFPWCGLLLDTRTLEVQSDYSSYARTSIRASLTF 960

Qy        961 NRGFKAGRNMRRKLFGVLRLKCHSLFLDLQVNSLQTVCTNIYKILLLQAYRFHACVLQLP 1020
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        961 NRGFKAGRNMRRKLFGVLRLKCHSLFLDLQVNSLQTVCTNIYKILLLQAYRFHACVLQLP 1020

Qy       1021 FHQQVWKNPTFFLRVISDTASLCYSILKAKNAGMSLGAKGAAGPLPSEAVQWLCHQAFLL 1080
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1021 FHQQVWKNPTFFLRVISDTASLCYSILKAKNAGMSLGAKGAAGPLPSEAVQWLCHQAFLL 1080

Qy       1081 KLTRHRVTYVPLLGSLRTAQTQLSRKLPGTTLTALEAAANPALPSDFKTILD 1132
              ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1081 KLTRHRVTYVPLLGSLRTAQTQLSRKLPGTTLTALEAAANPALPSDFKTILD 1132


RESULT 12
AAU72735
ID   AAU72735 standard; protein; 1132 AA.
XX
AC   AAU72735;
XX
DT   09-APR-2002  (first entry)
XX
DE   Human telomerase reverse transcriptase (TERT).
XX
KW   Telomerase reverse transcriptase; TERT; cytostatic; apoptosis;
KW   cell growth inhibitor; antisense oligonucleotide; antisense technology.
XX
OS   Homo sapiens.
XX
PN   WO200188198-A1.
XX
PD   22-NOV-2001.
XX
PF   15-MAY-2001; 2001WO-US015774.
XX
PR   16-MAY-2000; 2000US-00572423.
PR   07-DEC-2000; 2000US-00733294.
XX
PA   (ISIS-) ISIS PHARM INC.
XX
PI   Monia BP,  Gaarde WA,  Freier SM,  Wancewicz E;
XX
DR   WPI; 2002-075321/10.
DR   N-PSDB; AAS96607.
XX
PT   New compound targeted to nucleic acid molecule encoding telomerase
PT   transcriptase (TERT), which specifically hybridizes with and inhibits
PT   expression of TERT, useful for modulating apoptosis and inhibiting cell
PT   growth.
XX
PS   Disclosure; Page 100-105; 154pp; English.
XX
CC   The invention describes a compound, 8-50 nucleobases in length targeted
CC   to a nucleic acid molecule encoding human TERT (telomerase reverse
CC   transcriptase), where the compound specifically hybridises with and
CC   inhibits the expression of TERT. A series of oligonucleotides were
CC   designed to target different regions of the human TERT RNA. These were 20
CC   nucleotides in length and composed of a central gap region consisting of
CC   ten 2'-deoxynucleotides, flanked on both sides (5' and 3' directions) by
CC   five-nucleotide wings. The wings were composed of 2'-methoxyethyl (2'-
CC   MOE) nucleotides. The compounds were analysed for their effect on human
CC   TERT mRNA levels by reverse transcriptase (RT)-polymerase chain reaction
CC   (PCR). The compound is useful for inhibiting the expression of TERT in
CC   cells or tissues, for treating a human having disease or condition
CC   associated with TERT, for modulating apoptosis, for inhibiting cell
CC   growth (preferably, cancer cell growth), in antisense therapy and for
CC   diagnostics and therapeutics. This is the amino acid sequence of human
CC   telomerase reverse transcriptase (TERT), described in the method of the
CC   invention
XX
SQ   Sequence 1132 AA;

  Query Match             100.0%;  Score 5961;  DB 5;  Length 1132;
  Best Local Similarity   100.0%;  Pred. No. 0;
  Matches 1132;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 MPRAPRCRAVRSLLRSHYREVLPLATFVRRLGPQGWRLVQRGDPAAFRALVAQCLVCVPW 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 MPRAPRCRAVRSLLRSHYREVLPLATFVRRLGPQGWRLVQRGDPAAFRALVAQCLVCVPW 60

Qy         61 DARPPPAAPSFRQVSCLKELVARVLQRLCERGAKNVLAFGFALLDGARGGPPEAFTTSVR 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 DARPPPAAPSFRQVSCLKELVARVLQRLCERGAKNVLAFGFALLDGARGGPPEAFTTSVR 120

Qy        121 SYLPNTVTDALRGSGAWGLLLRRVGDDVLVHLLARCALFVLVAPSCAYQVCGPPLYQLGA 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 SYLPNTVTDALRGSGAWGLLLRRVGDDVLVHLLARCALFVLVAPSCAYQVCGPPLYQLGA 180

Qy        181 ATQARPPPHASGPRRRLGCERAWNHSVREAGVPLGLPAPGARRRGGSASRSLPLPKRPRR 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 ATQARPPPHASGPRRRLGCERAWNHSVREAGVPLGLPAPGARRRGGSASRSLPLPKRPRR 240

Qy        241 GAAPEPERTPVGQGSWAHPGRTRGPSDRGFCVVSPARPAEEATSLEGALSGTRHSHPSVG 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 GAAPEPERTPVGQGSWAHPGRTRGPSDRGFCVVSPARPAEEATSLEGALSGTRHSHPSVG 300

Qy        301 RQHHAGPPSTSRPPRPWDTPCPPVYAETKHFLYSSGDKEQLRPSFLLSSLRPSLTGARRL 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 RQHHAGPPSTSRPPRPWDTPCPPVYAETKHFLYSSGDKEQLRPSFLLSSLRPSLTGARRL 360

Qy        361 VETIFLGSRPWMPGTPRRLPRLPQRYWQMRPLFLELLGNHAQCPYGVLLKTHCPLRAAVT 420
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                 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        361 VETIFLGSRPWMPGTPRRLPRLPQRYWQMRPLFLELLGNHAQCPYGVLLKTHCPLRAAVT 420

Qy        421 PAAGVCAREKPQGSVAAPEEEDTDPRRLVQLLRQHSSPWQVYGFVRACLRRLVPPGLWGS 480
                 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        421 PAAGVCAREKPQGSVAAPEEEDTDPRRLVQLLRQHSSPWQVYGFVRACLRRLVPPGLWGS 480

Qy        481 RHNERRFLRNTKKFISLGKHAKLSLQELTWKMSVRDCAWLRRSPGVGCVPAAEHRLREEI 540
                 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        481 RHNERRFLRNTKKFISLGKHAKLSLQELTWKMSVRDCAWLRRSPGVGCVPAAEHRLREEI 540

Qy        541 LAKFLHWLMSVYVVELLRSFFYVTETTFQKNRLFFYRKSVWSKLQSIGIRQHLKRVQLRE 600
                 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        541 LAKFLHWLMSVYVVELLRSFFYVTETTFQKNRLFFYRKSVWSKLQSIGIRQHLKRVQLRE 600

Qy        601 LSEAEVRQHREARPALLTSRLRFIPKPDGLRPIVNMDYVVGARTFRREKRAERLTSRVKA 660
                 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        601 LSEAEVRQHREARPALLTSRLRFIPKPDGLRPIVNMDYVVGARTFRREKRAERLTSRVKA 660

Qy        661 LFSVLNYERARRPGLLGASVLGLDDIHRAWRTFVLRVRAQDPPPELYFVKVDVTGAYDTI 720
                 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        661 LFSVLNYERARRPGLLGASVLGLDDIHRAWRTFVLRVRAQDPPPELYFVKVDVTGAYDTI 720

Qy        721 PQDRLTEVIASIIKPQNTYCVRRYAVVQKAAHGHVRKAFKSHVSTLTDLQPYMRQFVAHL 780
                 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        721 PQDRLTEVIASIIKPQNTYCVRRYAVVQKAAHGHVRKAFKSHVSTLTDLQPYMRQFVAHL 780

Qy        781 QETSPLRDAVVIEQSSSLNEASSGLFDVFLRFMCHHAVRIRGKSYVQCQGIPQGSILSTL 840
                 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        781 QETSPLRDAVVIEQSSSLNEASSGLFDVFLRFMCHHAVRIRGKSYVQCQGIPQGSILSTL 840

Qy        841 LCSLCYGDMENKLFAGIRRDGLLLRLVDDFLLVTPHLTHAKTFLRTLVRGVPEYGCVVNL 900
                 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        841 LCSLCYGDMENKLFAGIRRDGLLLRLVDDFLLVTPHLTHAKTFLRTLVRGVPEYGCVVNL 900

Qy        901 RKTVVNFPVEDEALGGTAFVQMPAHGLFPWCGLLLDTRTLEVQSDYSSYARTSIRASLTF 960
                 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        901 RKTVVNFPVEDEALGGTAFVQMPAHGLFPWCGLLLDTRTLEVQSDYSSYARTSIRASLTF 960

Qy        961 NRGFKAGRNMRRKLFGVLRLKCHSLFLDLQVNSLQTVCTNIYKILLLQAYRFHACVLQLP 1020
                 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        961 NRGFKAGRNMRRKLFGVLRLKCHSLFLDLQVNSLQTVCTNIYKILLLQAYRFHACVLQLP 1020

Qy       1021 FHQQVWKNPTFFLRVISDTASLCYSILKAKNAGMSLGAKGAAGPLPSEAVQWLCHQAFLL 1080
                 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1021 FHQQVWKNPTFFLRVISDTASLCYSILKAKNAGMSLGAKGAAGPLPSEAVQWLCHQAFLL 1080

Qy       1081 KLTRHRVTYVPLLGSLRTAQTQLSRKLPGTTLTALEAAANPALPSDFKTILD 1132
                 |||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1081 KLTRHRVTYVPLLGSLRTAQTQLSRKLPGTTLTALEAAANPALPSDFKTILD 1132
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RESULT 13
ABR42384
ID ABR42384 standard; protein; 1132 AA.
XX
AC ABR42384;
XX
DT 11-AUG-2003 (first entry)
XX
DE Human telomerase reverse transcriptase.
XX
KW Telomerase reverse transcriptase; TERT; enzyme; RNA interference;
KW short interfering RNA; siRNA; cancer; tumour; cytostatic; contraceptive;
KW immunosuppressive; antiinfertility; fungicide; antiparasitic;
KW antiinflammatory; human; gene therapy.
XX
OS Homo sapiens.
XX
PN WO2003035667-A2.
XX
PD 01-MAY-2003.
XX
PF 16-OCT-2002; 2002WO-US033065.
XX
PR 22-OCT-2001; 2001US-0345326P.
PR 20-FEB-2002; 2002US-0359196P.
PR 22-MAY-2002; 2002US-0383195P.
XX
PA (UYRP) UNIV ROCHESTER.
XX
PI Rowley PT;
XX
DR WPI; 2003-403336/38.
DR N-PSDB; ACC58039.
XX
PT Novel double-stranded short interfering RNA having sense and antisense
PT nucleic acids which are complementary to each other and to target nucleic
PT acid e.g., telomerase RNA or mRNA encoding telomerase reverse
PT transcriptase.
XX
PS Disclosure; Fig 4; 37pp; English.
XX
CC The present sequence is the protein sequence of human telomerase reverse
CC transcriptase (TERT). The invention relates to the discovery that double-
CC stranded interfering RNAs, such as short interfering RNAs (siRNA), which
CC target telomerase RNA or TERT mRNA are capable of inhibiting telomerase
CC activity. Inhibition of telomerase in cancer cells leads to telomere
CC shortening, end-to-end chromosomal fusion, and apoptosis. Interference of
CC telomerase activity can also be used for treatment of infertility, for
CC contraception or sterilisation, for immunosuppression, for treatment of
CC yeast, parasite and fungal infections, and in antiinflammatory therapies.
CC As telomerase is active in a limited number of cell types, e.g. tumour
CC cells, germline cells, certain stem cells of the haematopoietic system, T
CC and B cells, sun-damaged skin, and proliferative cervix, most normal
CC cells are not affected by telomerase RNA interference therapy
XX
SQ Sequence 1132 AA;

Query Match 100.0%; Score 5961; DB 6; Length 1132;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1132; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy          1 MPRAPRCRAVRSLLRSHYREVLPLATFVRRLGPQGWRLVQRGDPAAFRALVAQCLVCVPW 60
                 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 MPRAPRCRAVRSLLRSHYREVLPLATFVRRLGPQGWRLVQRGDPAAFRALVAQCLVCVPW 60

Qy         61 DARPPPAAPSFRQVSCLKELVARVLQRLCERGAKNVLAFGFALLDGARGGPPEAFTTSVR 120
                 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 DARPPPAAPSFRQVSCLKELVARVLQRLCERGAKNVLAFGFALLDGARGGPPEAFTTSVR 120

Qy        121 SYLPNTVTDALRGSGAWGLLLRRVGDDVLVHLLARCALFVLVAPSCAYQVCGPPLYQLGA 180
                 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 SYLPNTVTDALRGSGAWGLLLRRVGDDVLVHLLARCALFVLVAPSCAYQVCGPPLYQLGA 180

Qy        181 ATQARPPPHASGPRRRLGCERAWNHSVREAGVPLGLPAPGARRRGGSASRSLPLPKRPRR 240
                 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 ATQARPPPHASGPRRRLGCERAWNHSVREAGVPLGLPAPGARRRGGSASRSLPLPKRPRR 240

Qy        241 GAAPEPERTPVGQGSWAHPGRTRGPSDRGFCVVSPARPAEEATSLEGALSGTRHSHPSVG 300
                 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 GAAPEPERTPVGQGSWAHPGRTRGPSDRGFCVVSPARPAEEATSLEGALSGTRHSHPSVG 300

Qy        301 RQHHAGPPSTSRPPRPWDTPCPPVYAETKHFLYSSGDKEQLRPSFLLSSLRPSLTGARRL 360
                 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 RQHHAGPPSTSRPPRPWDTPCPPVYAETKHFLYSSGDKEQLRPSFLLSSLRPSLTGARRL 360

Qy        361 VETIFLGSRPWMPGTPRRLPRLPQRYWQMRPLFLELLGNHAQCPYGVLLKTHCPLRAAVT 420
                 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        361 VETIFLGSRPWMPGTPRRLPRLPQRYWQMRPLFLELLGNHAQCPYGVLLKTHCPLRAAVT 420

Qy        421 PAAGVCAREKPQGSVAAPEEEDTDPRRLVQLLRQHSSPWQVYGFVRACLRRLVPPGLWGS 480
                 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        421 PAAGVCAREKPQGSVAAPEEEDTDPRRLVQLLRQHSSPWQVYGFVRACLRRLVPPGLWGS 480

Qy        481 RHNERRFLRNTKKFISLGKHAKLSLQELTWKMSVRDCAWLRRSPGVGCVPAAEHRLREEI 540
```

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                 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        481 RHNERRFLRNTKKFISLGKHAKLSLQELTWKMSVRDCAWLRRSPGVGCVPAAEHRLREEI 540

Qy        541 LAKFLHWLMSVYVVELLRSFFYVTETTFQKNRLFFYRKSVWSKLQSIGIRQHLKRVQLRE 600
                 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        541 LAKFLHWLMSVYVVELLRSFFYVTETTFQKNRLFFYRKSVWSKLQSIGIRQHLKRVQLRE 600

Qy        601 LSEAEVRQHREARPALLTSRLRFIPKPDGLRPIVNMDYVVGARTFRREKRAERLTSRVKA 660
                 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        601 LSEAEVRQHREARPALLTSRLRFIPKPDGLRPIVNMDYVVGARTFRREKRAERLTSRVKA 660

Qy        661 LFSVLNYERARRPGLLGASVLGLDDIHRAWRTFVLRVRAQDPPPELYFVKVDVTGAYDTI 720
                 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        661 LFSVLNYERARRPGLLGASVLGLDDIHRAWRTFVLRVRAQDPPPELYFVKVDVTGAYDTI 720

Qy        721 PQDRLTEVIASIIKPQNTYCVRRYAVVQKAAHGHVRKAFKSHVSTLTDLQPYMRQFVAHL 780
                 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        721 PQDRLTEVIASIIKPQNTYCVRRYAVVQKAAHGHVRKAFKSHVSTLTDLQPYMRQFVAHL 780

Qy        781 QETSPLRDAVVIEQSSSLNEASSGLFDVFLRFMCHHAVRIRGKSYVQCQGIPQGSILSTL 840
                 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        781 QETSPLRDAVVIEQSSSLNEASSGLFDVFLRFMCHHAVRIRGKSYVQCQGIPQGSILSTL 840

Qy        841 LCSLCYGDMENKLFAGIRRDGLLLRLVDDFLLVTPHLTHAKTFLRTLVRGVPEYGCVVNL 900
                 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        841 LCSLCYGDMENKLFAGIRRDGLLLRLVDDFLLVTPHLTHAKTFLRTLVRGVPEYGCVVNL 900

Qy        901 RKTVVNFPVEDEALGGTAFVQMPAHGLFPWCGLLLDTRTLEVQSDYSSYARTSIRASLTF 960
                 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        901 RKTVVNFPVEDEALGGTAFVQMPAHGLFPWCGLLLDTRTLEVQSDYSSYARTSIRASLTF 960

Qy        961 NRGFKAGRNMRRKLFGVLRLKCHSLFLDLQVNSLQTVCTNIYKILLLQAYRFHACVLQLP 1020
                 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        961 NRGFKAGRNMRRKLFGVLRLKCHSLFLDLQVNSLQTVCTNIYKILLLQAYRFHACVLQLP 1020

Qy       1021 FHQQVWKNPTFFLRVISDTASLCYSILKAKNAGMSLGAKGAAGPLPSEAVQWLCHQAFLL 1080
                 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1021 FHQQVWKNPTFFLRVISDTASLCYSILKAKNAGMSLGAKGAAGPLPSEAVQWLCHQAFLL 1080

Qy       1081 KLTRHRVTYVPLLGSLRTAQTQLSRKLPGTTLTALEAAANPALPSDFKTILD 1132
                 ||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1081 KLTRHRVTYVPLLGSLRTAQTQLSRKLPGTTLTALEAAANPALPSDFKTILD 1132
```

RESULT 14
ABR42063
ID ABR42063 standard; protein; 1132 AA.
XX
AC ABR42063;
XX
DT 28-JUL-2003 (first entry)
XX
DE Human telomerase reverse transcriptase.
XX
KW Telomerase reverse transcriptase; TERT: enzyme; RNA interference;
KW short interfering RNA; siRNA; cancer; tumour; cytostatic; contraceptive;
KW immunosuppressive; antiinfertility; fungicide; antiparasitic;
KW antiinflammatory; human; gene therapy.
XX
OS Homo sapiens.
XX
PN WO2003034985-A2.
XX
PD 01-MAY-2003.
XX
PF 16-OCT-2002; 2002WO-US033146.
XX
PR 22-OCT-2001; 2001US-0345326P.
PR 20-FEB-2002; 2002US-0359196P.
PR 22-MAY-2002; 2002US-0383195P.
XX
PA (UYRP) UNIV ROCHESTER.
XX
PI Rowley PT;
XX
DR WPI; 2003-403289/38.
DR N-PSDB; ACC57552.
XX
PT Novel nucleic acid encoding or comprising interfering RNAs which target
PT telomerase RNA, useful for inhibiting telomerase activity for treating
PT cancer, infertility and disorders of the immune system.
XX
PS Disclosure; Fig 4; 52pp; English.
XX
CC The present sequence is that of human telomerase reverse transcriptase
CC (TERT). The invention relates to the discovery that double-stranded
CC interfering RNAs, such as short interfering RNAs (siRNA), which target
CC telomerase RNA or TERT mRNA are capable of inhibiting telomerase
CC activity. Inhibition of telomerase in cancer cells leads to telomere
CC shortening, end-to-end chromosomal fusion, and apoptosis. Interference of
CC telomerase activity can also be used for treatment of infertility, for
CC contraception or sterilisation, for immunosuppression, for treatment of
CC yeast, parasite and fungal infections, and in antiinflammatory therapies.
CC As telomerase is active in a limited number of cell types, e.g. tumour
CC cells, germline cells, certain stem cells of the haematopoietic system, T
CC and B cells, sun-damaged skin, and proliferative cervix, most normal
CC cells are not affected by telomerase RNA interference therapy
XX
SQ Sequence 1132 AA;

Query Match 100.0%; Score 5961; DB 6; Length 1132;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1132; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```
Qy          1 MPRAPRCRAVRSLLRSHYREVLPLATFVRRLGPQGWRLVQRGDPAAFRALVAQCLVCVPW 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 MPRAPRCRAVRSLLRSHYREVLPLATFVRRLGPQGWRLVQRGDPAAFRALVAQCLVCVPW 60

Qy         61 DARPPPAAPSFRQVSCLKELVARVLQRLCERGAKNVLAFGFALLDGARGGPPEAFTTSVR 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 DARPPPAAPSFRQVSCLKELVARVLQRLCERGAKNVLAFGFALLDGARGGPPEAFTTSVR 120

Qy        121 SYLPNTVTDALRGSGAWGLLLRRVGDDVLVHLLARCALFVLVAPSCAYQVCGPPLYQLGA 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 SYLPNTVTDALRGSGAWGLLLRRVGDDVLVHLLARCALFVLVAPSCAYQVCGPPLYQLGA 180

Qy        181 ATQARPPPHASGPRRRLGCERAWNHSVREAGVPLGLPAPGARRRGGSASRSLPLPKRPRR 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 ATQARPPPHASGPRRRLGCERAWNHSVREAGVPLGLPAPGARRRGGSASRSLPLPKRPRR 240

Qy        241 GAAPEPERTPVGQGSWAHPGRTRGPSDRGFCVVSPARPAEEATSLEGALSGTRHSHPSVG 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 GAAPEPERTPVGQGSWAHPGRTRGPSDRGFCVVSPARPAEEATSLEGALSGTRHSHPSVG 300

Qy        301 RQHHAGPPSTSRPPRPWDTPCPPVYAETKHFLYSSGDKEQLRPSFLLSSLRPSLTGARRL 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 RQHHAGPPSTSRPPRPWDTPCPPVYAETKHFLYSSGDKEQLRPSFLLSSLRPSLTGARRL 360

Qy        361 VETIFLGSRPWMPGTPRRLPRLPQRYWQMRPLFLELLGNHAQCPYGVLLKTHCPLRAAVT 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        361 VETIFLGSRPWMPGTPRRLPRLPQRYWQMRPLFLELLGNHAQCPYGVLLKTHCPLRAAVT 420

Qy        421 PAAGVCAREKPQGSVAAPEEEDTDPRRLVQLLRQHSSPWQVYGFVRACLRRLVPPGLWGS 480
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        421 PAAGVCAREKPQGSVAAPEEEDTDPRRLVQLLRQHSSPWQVYGFVRACLRRLVPPGLWGS 480

Qy        481 RHNERRFLRNTKKFISLGKHAKLSLQELTWKMSVRDCAWLRRSPGVGCVPAAEHRLREEI 540
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        481 RHNERRFLRNTKKFISLGKHAKLSLQELTWKMSVRDCAWLRRSPGVGCVPAAEHRLREEI 540

Qy        541 LAKFLHWLMSVYVVELLRSFFYVTETTFQKNRLFFYRKSVWSKLQSIGIRQHLKRVQLRE 600
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        541 LAKFLHWLMSVYVVELLRSFFYVTETTFQKNRLFFYRKSVWSKLQSIGIRQHLKRVQLRE 600

Qy        601 LSEAEVRQHREARPALLTSRLRFIPKPDGLRPIVNMDYVVGARTFRREKRAERLTSRVKA 660
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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Db        601 LSEAEVRQHREARPALLTSRLRFIPKPDGLRPIVNMDYVVGARTFRREKRAERLTSRVKA 660

Qy        661 LFSVLNYERARRPGLLGASVLGLDDIHRAWRTFVLRVRAQDPPPELYFVKVDVTGAYDTI 720
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        661 LFSVLNYERARRPGLLGASVLGLDDIHRAWRTFVLRVRAQDPPPELYFVKVDVTGAYDTI 720

Qy        721 PQDRLTEVIASIIKPQNTYCVRRYAVVQKAAHGHVRKAFKSHVSTLTDLQPYMRQFVAHL 780
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        721 PQDRLTEVIASIIKPQNTYCVRRYAVVQKAAHGHVRKAFKSHVSTLTDLQPYMRQFVAHL 780

Qy        781 QETSPLRDAVVIEQSSSLNEASSGLFDVFLRFMCHHAVRIRGKSYVQCQGIPQGSILSTL 840
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        781 QETSPLRDAVVIEQSSSLNEASSGLFDVFLRFMCHHAVRIRGKSYVQCQGIPQGSILSTL 840

Qy        841 LCSLCYGDMENKLFAGIRRDGLLLRLVDDFLLVTPHLTHAKTFLRTLVRGVPEYGCVVNL 900
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        841 LCSLCYGDMENKLFAGIRRDGLLLRLVDDFLLVTPHLTHAKTFLRTLVRGVPEYGCVVNL 900

Qy        901 RKTVVNFPVEDEALGGTAFVQMPAHGLFPWCGLLLDTRTLEVQSDYSSYARTSIRASLTF 960
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        901 RKTVVNFPVEDEALGGTAFVQMPAHGLFPWCGLLLDTRTLEVQSDYSSYARTSIRASLTF 960

Qy        961 NRGFKAGRNMRRKLFGVLRLKCHSLFLDLQVNSLQTVCTNIYKILLLQAYRFHACVLQLP 1020
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        961 NRGFKAGRNMRRKLFGVLRLKCHSLFLDLQVNSLQTVCTNIYKILLLQAYRFHACVLQLP 1020

Qy       1021 FHQQVWKNPTFFLRVISDTASLCYSILKAKNAGMSLGAKGAAGPLPSEAVQWLCHQAFLL 1080
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1021 FHQQVWKNPTFFLRVISDTASLCYSILKAKNAGMSLGAKGAAGPLPSEAVQWLCHQAFLL 1080

Qy       1081 KLTRHRVTYVPLLGSLRTAQTQLSRKLPGTTLTALEAAANPALPSDFKTILD 1132
              |||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1081 KLTRHRVTYVPLLGSLRTAQTQLSRKLPGTTLTALEAAANPALPSDFKTILD 1132
```

RESULT 15
ABP56676
ID ABP56676 standard; protein; 1132 AA.
XX
AC ABP56676;
XX
DT 25-MAR-2003 (first entry)
XX
DE Human telomerase reverse transcriptase protein SEQ ID NO:2.
XX
KW Human; telomerase reverse transcriptase; enzyme; hTERT; chromosome 5;
KW vulnerary; antiulcer; epithelial cell migration promoter; wound;
KW epithelisation; skin wound; lesion; burn; surgical incision; ulcer;
KW epithelial cell; keratinocyte; epidermal; mucosal.
XX
OS Homo sapiens.
XX
PN WO200291999-A2.
XX
PD 21-NOV-2002.
XX
PF 09-MAY-2002; 2002WO-US014867.
XX
PR 09-MAY-2001; 2001US-0289903P.
XX
PA (GERO-) GERON CORP.
XX
PI Jiang X, Chiu C, Harley CB;
XX
DR WPI; 2003-120591/11.
DR N-PSDB; ABZ22474.
XX
PT Composition for treating wounds and enhancing epithelization of a skin
PT surface, comprises vector encoding telomerase reverse transcriptase or
PT telomerized epithelial cells on a microparticle or a matrix.
XX
PS Disclosure; Page 32; 68pp; English.
XX

CC The present invention describes a pharmaceutical composition (I)
CC comprising a vector encoding telomerase reverse transcriptase (TERT) in
CC an excipient or device, or comprises telomerised epithelial cells on a
CC microparticle or a matrix suitable for topical administration or
CC administration to a wound site. (I) has vulnerary and antiulcer
CC activities and can be used to promote epithelial cell migration. (I) is
CC useful for treating a wound and enhancing epithelisation of a skin
CC surface. The wound is especially skin wound including acute lesion such
CC as traumatic lesion, burn, or surgical incision, chronic lesion such as
CC chronic venous ulcer, diabetic ulcer or compression ulcer and the wound
CC is further monitored for closure. The telomerase activity or TERT
CC expression is increased in epithelial cells at the site of treatment and
CC also in fibroblasts or endothelial cells at the site of treatment. The
CC epithelial cells are especially keratinocytes. A polynucleotide encoding
CC TERT is useful for the preparation of a medicament for treatment of a
CC wound or an epithelial surface in a human or animal. An epithelial cell
CC with increased telomerase activity or increased expression of TERT is
CC useful for preparation of a medicament for the treatment of a wound in a
CC human or animal. (I) is also useful for treating wounds of other
CC epidermal surfaces including mucosal surfaces such as bronchus, mouth,
CC nose, oesophagus, stomach, or intestine. The present sequence represents
CC human TERT (hTERT), which is given in the exemplification of the present
CC invention. hTERT is located to chromosome 5
XX
SQ Sequence 1132 AA;

Query Match 100.0%; Score 5961; DB 6; Length 1132;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1132; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```
Qy          1 MPRAPRCRAVRSLLRSHYREVLPLATFVRRLGPQGWRLVQRGDPAAFRALVAQCLVCVPW 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 MPRAPRCRAVRSLLRSHYREVLPLATFVRRLGPQGWRLVQRGDPAAFRALVAQCLVCVPW 60

Qy         61 DARPPPAAPSFRQVSCLKELVARVLQRLCERGAKNVLAFGFALLDGARGGPPEAFTTSVR 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 DARPPPAAPSFRQVSCLKELVARVLQRLCERGAKNVLAFGFALLDGARGGPPEAFTTSVR 120

Qy        121 SYLPNTVTDALRGSGAWGLLLRRVGDDVLVHLLARCALFVLVAPSCAYQVCGPPLYQLGA 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 SYLPNTVTDALRGSGAWGLLLRRVGDDVLVHLLARCALFVLVAPSCAYQVCGPPLYQLGA 180

Qy        181 ATQARPPPHASGPRRRLGCERAWNHSVREAGVPLGLPAPGARRRGGSASRSLPLPKRPRR 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 ATQARPPPHASGPRRRLGCERAWNHSVREAGVPLGLPAPGARRRGGSASRSLPLPKRPRR 240

Qy        241 GAAPEPERTPVGQGSWAHPGRTRGPSDRGFCVVSPARPAEEATSLEGALSGTRHSHPSVG 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 GAAPEPERTPVGQGSWAHPGRTRGPSDRGFCVVSPARPAEEATSLEGALSGTRHSHPSVG 300

Qy        301 RQHHAGPPSTSRPPRPWDTPCPPVYAETKHFLYSSGDKEQLRPSFLLSSLRPSLTGARRL 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 RQHHAGPPSTSRPPRPWDTPCPPVYAETKHFLYSSGDKEQLRPSFLLSSLRPSLTGARRL 360

Qy        361 VETIFLGSRPWMPGTPRRLPRLPQRYWQMRPLFLELLGNHAQCPYGVLLKTHCPLRAAVT 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        361 VETIFLGSRPWMPGTPRRLPRLPQRYWQMRPLFLELLGNHAQCPYGVLLKTHCPLRAAVT 420

Qy        421 PAAGVCAREKPQGSVAAPEEEDTDPRRLVQLLRQHSSPWQVYGFVRACLRRLVPPGLWGS 480
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        421 PAAGVCAREKPQGSVAAPEEEDTDPRRLVQLLRQHSSPWQVYGFVRACLRRLVPPGLWGS 480

Qy        481 RHNERRFLRNTKKFISLGKHAKLSLQELTWKMSVRDCAWLRRSPGVGCVPAAEHRLREEI 540
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        481 RHNERRFLRNTKKFISLGKHAKLSLQELTWKMSVRDCAWLRRSPGVGCVPAAEHRLREEI 540

Qy        541 LAKFLHWLMSVYVVELLRSFFYVTETTFQKNRLFFYRKSVWSKLQSIGIRQHLKRVQLRE 600
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        541 LAKFLHWLMSVYVVELLRSFFYVTETTFQKNRLFFYRKSVWSKLQSIGIRQHLKRVQLRE 600

Qy        601 LSEAEVRQHREARPALLTSRLRFIPKPDGLRPIVNMDYVVGARTFRREKRAERLTSRVKA 660
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        601 LSEAEVRQHREARPALLTSRLRFIPKPDGLRPIVNMDYVVGARTFRREKRAERLTSRVKA 660
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```
Qy        661 LFSVLNYERARRPGLLGASVLGLDDIHRAWRTFVLRVRAQDPPPELYFVKVDVTGAYDTI 720
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        661 LFSVLNYERARRPGLLGASVLGLDDIHRAWRTFVLRVRAQDPPPELYFVKVDVTGAYDTI 720

Qy        721 PQDRLTEVIASIIKPQNTYCVRRYAVVQKAAHGHVRKAFKSHVSTLTDLQPYMRQFVAHL 780
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        721 PQDRLTEVIASIIKPQNTYCVRRYAVVQKAAHGHVRKAFKSHVSTLTDLQPYMRQFVAHL 780

Qy        781 QETSPLRDAVVIEQSSSLNEASSGLFDVFLRFMCHHAVRIRGKSYVQCQGIPQGSILSTL 840
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        781 QETSPLRDAVVIEQSSSLNEASSGLFDVFLRFMCHHAVRIRGKSYVQCQGIPQGSILSTL 840

Qy        841 LCSLCYGDMENKLFAGIRRDGLLLRLVDDFLLVTPHLTHAKTFLRTLVRGVPEYGCVVNL 900
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        841 LCSLCYGDMENKLFAGIRRDGLLLRLVDDFLLVTPHLTHAKTFLRTLVRGVPEYGCVVNL 900

Qy        901 RKTVVNFPVEDEALGGTAFVQMPAHGLFPWCGLLLDTRTLEVQSDYSSYARTSIRASLTF 960
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        901 RKTVVNFPVEDEALGGTAFVQMPAHGLFPWCGLLLDTRTLEVQSDYSSYARTSIRASLTF 960

Qy        961 NRGFKAGRNMRRKLFGVLRLKCHSLFLDLQVNSLQTVCTNIYKILLLQAYRFHACVLQLP 1020
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        961 NRGFKAGRNMRRKLFGVLRLKCHSLFLDLQVNSLQTVCTNIYKILLLQAYRFHACVLQLP 1020

Qy       1021 FHQQVWKNPTFFLRVISDTASLCYSILKAKNAGMSLGAKGAAGPLPSEAVQWLCHQAFLL 1080
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1021 FHQQVWKNPTFFLRVISDTASLCYSILKAKNAGMSLGAKGAAGPLPSEAVQWLCHQAFLL 1080

Qy       1081 KLTRHRVTYVPLLGSLRTAQTQLSRKLPGTTLTALEAAANPALPSDFKTILD 1132
              |||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1081 KLTRHRVTYVPLLGSLRTAQTQLSRKLPGTTLTALEAAANPALPSDFKTILD 1132
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RESULT 16
ABR58045
ID ABR58045 standard; protein; 1132 AA.
XX
AC ABR58045;
XX
DT 29-AUG-2003 (first entry)
XX
DE Human telomerase reverse transcriptase.
XX
KW Enzyme; human; telomerase reverse transcriptase; adipogenic capacity;
KW primary preadipocyte cell; adipogenesis; obesity; adipocytokine;
KW anorectic; adiponectin; insulin.
XX
OS Homo sapiens.
XX
PN WO2003031640-A2.
XX
PD 17-APR-2003.
XX
PF 07-OCT-2002; 2002WO-US031635.
XX
PR 06-OCT-2001; 2001US-0327650P.
PR 06-OCT-2001; 2001US-0327651P.
XX
PA (BOST-) BOSTON MEDICAL CENT CORP.
XX
PI Kirkland J, Tchkonia T;
XX
DR WPI; 2003-421278/39.
DR N-PSDB; ACC44482.
XX
PT New primary preadipocyte strain expressing telomerase reverse
PT transcriptase, useful in research applications, screening assays,
PT clinical applications, and in the administration of therapeutic agents,
PT particularly for obesity.
XX
PS Disclosure; Page 13; 53pp; English.
XX
CC The invention relates to the generation of primary preadipocyte cell
CC strains that expresse telomerase reverse transcriptase (TERT- the
CC catalytic subunit of telomerase), and maintain and/or enhance replicative
CC potential and maintain adipogenic capacity of the cell. This sequence
CC represents the TERT protein. The cell strain can be used in research to
CC study all aspect of adipogenesis, especially in relation to researching
CC treatments for e.g. obesity. The cell can also be used to identify
CC adipogenesis modulators for use as therapeutic agents such as hormones,
CC growth factors, cytokines, enzymes, cholesterol binding proteins,
CC cholesterol removing proteins or their combinations. Alternatively, the
CC therapeutic agent may be an adipocytokine, preferably adiponectin, or
CC insulin
XX
SQ Sequence 1132 AA;

Query Match 100.0%; Score 5961; DB 6; Length 1132;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1132; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy          1 MPRAPRCRAVRSLLRSHYREVLPLATFVRRLGPQGWRLVQRGDPAAFRALVAQCLVCVPW 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 MPRAPRCRAVRSLLRSHYREVLPLATFVRRLGPQGWRLVQRGDPAAFRALVAQCLVCVPW 60

Qy         61 DARPPPAAPSFRQVSCLKELVARVLQRLCERGAKNVLAFGFALLDGARGGPPEAFTTSVR 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 DARPPPAAPSFRQVSCLKELVARVLQRLCERGAKNVLAFGFALLDGARGGPPEAFTTSVR 120

Qy        121 SYLPNTVTDALRGSGAWGLLLRRVGDDVLVHLLARCALFVLVAPSCAYQVCGPPLYQLGA 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 SYLPNTVTDALRGSGAWGLLLRRVGDDVLVHLLARCALFVLVAPSCAYQVCGPPLYQLGA 180

Qy        181 ATQARPPPHASGPRRRLGCERAWNHSVREAGVPLGLPAPGARRRGGSASRSLPLPKRPRR 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 ATQARPPPHASGPRRRLGCERAWNHSVREAGVPLGLPAPGARRRGGSASRSLPLPKRPRR 240

Qy        241 GAAPEPERTPVGQGSWAHPGRTRGPSDRGFCVVSPARPAEEATSLEGALSGTRHSHPSVG 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 GAAPEPERTPVGQGSWAHPGRTRGPSDRGFCVVSPARPAEEATSLEGALSGTRHSHPSVG 300

Qy        301 RQHHAGPPSTSRPPRPWDTPCPPVYAETKHFLYSSGDKEQLRPSFLLSSLRPSLTGARRL 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 RQHHAGPPSTSRPPRPWDTPCPPVYAETKHFLYSSGDKEQLRPSFLLSSLRPSLTGARRL 360

Qy        361 VETIFLGSRPWMPGTPRRLPRLPQRYWQMRPLFLELLGNHAQCPYGVLLKTHCPLRAAVT 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        361 VETIFLGSRPWMPGTPRRLPRLPQRYWQMRPLFLELLGNHAQCPYGVLLKTHCPLRAAVT 420

Qy        421 PAAGVCAREKPQGSVAAPEEEDTDPRRLVQLLRQHSSPWQVYGFVRACLRRLVPPGLWGS 480
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        421 PAAGVCAREKPQGSVAAPEEEDTDPRRLVQLLRQHSSPWQVYGFVRACLRRLVPPGLWGS 480

Qy        481 RHNERRFLRNTKKFISLGKHAKLSLQELTWKMSVRDCAWLRRSPGVGCVPAAEHRLREEI 540
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        481 RHNERRFLRNTKKFISLGKHAKLSLQELTWKMSVRDCAWLRRSPGVGCVPAAEHRLREEI 540

Qy        541 LAKFLHWLMSVYVVELLRSFFYVTETTFQKNRLFFYRKSVWSKLQSIGIRQHLKRVQLRE 600
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        541 LAKFLHWLMSVYVVELLRSFFYVTETTFQKNRLFFYRKSVWSKLQSIGIRQHLKRVQLRE 600

Qy        601 LSEAEVRQHREARPALLTSRLRFIPKPDGLRPIVNMDYVVGARTFRREKRAERLTSRVKA 660
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        601 LSEAEVRQHREARPALLTSRLRFIPKPDGLRPIVNMDYVVGARTFRREKRAERLTSRVKA 660

Qy        661 LFSVLNYERARRPGLLGASVLGLDDIHRAWRTFVLRVRAQDPPPELYFVKVDVTGAYDTI 720
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        661 LFSVLNYERARRPGLLGASVLGLDDIHRAWRTFVLRVRAQDPPPELYFVKVDVTGAYDTI 720

Qy        721 PQDRLTEVIASIIKPQNTYCVRRYAVVQKAAHGHVRKAFKSHVSTLTDLQPYMRQFVAHL 780
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        721 PQDRLTEVIASIIKPQNTYCVRRYAVVQKAAHGHVRKAFKSHVSTLTDLQPYMRQFVAHL 780

Qy        781 QETSPLRDAVVIEQSSSLNEASSGLFDVFLRFMCHHAVRIRGKSYVQCQGIPQGSILSTL 840
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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Db        781 QETSPLRDAVVIEQSSSLNEASSGLFDVFLRFMCHHAVRIRGKSYVQCQGIPQGSILSTL 840

Qy        841 LCSLCYGDMENKLFAGIRRDGLLLRLVDDFLLVTPHLTHAKTFLRTLVRGVPEYGCVVNL 900
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        841 LCSLCYGDMENKLFAGIRRDGLLLRLVDDFLLVTPHLTHAKTFLRTLVRGVPEYGCVVNL 900

Qy        901 RKTVVNFPVEDEALGGTAFVQMPAHGLFPWCGLLLDTRTLEVQSDYSSYARTSIRASLTF 960
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        901 RKTVVNFPVEDEALGGTAFVQMPAHGLFPWCGLLLDTRTLEVQSDYSSYARTSIRASLTF 960

Qy        961 NRGFKAGRNMRRKLFGVLRLKCHSLFLDLQVNSLQTVCTNIYKILLLQAYRFHACVLQLP 1020
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        961 NRGFKAGRNMRRKLFGVLRLKCHSLFLDLQVNSLQTVCTNIYKILLLQAYRFHACVLQLP 1020

Qy       1021 FHQQVWKNPTFFLRVISDTASLCYSILKAKNAGMSLGAKGAAGPLPSEAVQWLCHQAFLL 1080
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1021 FHQQVWKNPTFFLRVISDTASLCYSILKAKNAGMSLGAKGAAGPLPSEAVQWLCHQAFLL 1080

Qy       1081 KLTRHRVTYVPLLGSLRTAQTQLSRKLPGTTLTALEAAANPALPSDFKTILD 1132
              |||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1081 KLTRHRVTYVPLLGSLRTAQTQLSRKLPGTTLTALEAAANPALPSDFKTILD 1132
```

RESULT 17
ADD21420
ID ADD21420 standard; protein; 1132 AA.
XX
AC ADD21420;
XX
DT 15-JAN-2004 (first entry)
XX
DE Human TERT protein related to continual cell growth.
XX
KW continual growth; cultured cell; cyclin dependent kinase; cdk4; cdk2;
KW cdk6; activating mutation; cell growth; cell division; cell cycle;
KW cancer-causing agent; continual growth-induced cell; enzyme; TERT;
KW telomerase; human.
XX
OS Homo sapiens.
XX
PN WO2003044169-A2.
XX
PD 30-MAY-2003.
XX
PF 15-NOV-2002; 2002WO-US036729.
XX
PR 15-NOV-2001; 2001US-0334760P.
XX
PA (UTEM) UNIV TEMPLE.
XX
PI Reddy PE, Rane SG, Mettus RV;
XX
DR WPI; 2003-449813/42.
XX
PT A composition for reversibly inducing continual growth in normal cells
PT comprises a cyclin dependent kinase protein (e.g. cdk4, cdk2 or cdk6) or
PT its active fragment, derivative, homolog or analog, having an activating
PT mutation.
XX
PS Claim 16; Page 135-138; 77pp; English.
XX
CC This invention relates to a novel composition for inducing a reversible
CC state of a continual growth in cultured cells and comprises at least one
CC compound comprising a cyclin dependent kinase (cdk)4, cdk2 or cdk6
CC protein having an activating mutation. Growth and division of living
CC cells involve a regular series of events and processes that comprise the
CC cell cycle. Cyclin dependent kinases cdk2, cdk4 and cdk6 are involved in
CC the control of G1, the point at which cells irrevocably commit to DNA
CC synthesis and thus enter the cell cycle. The invention is useful in
CC reversibly inducing continual growth in normal cells and may allow the
CC screening of cancer-causing agents with the continual growth-induced
CC cells. The present sequence is that of the human TERT protein, the
CC catalytic subunit of telomerase, related to the invention. Note: Due to
CC an error in the specification or sequence listing, the Seq ID numbers
CC given in the disclosure do not correspond to those given in the sequence
CC listing. It is therefore unclear which Seq ID number corresponds to which
CC sequence and exactly which sequence is being claimed.
XX
SQ Sequence 1132 AA;

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  Query Match             100.0%;  Score 5961;  DB 7;  Length 1132;
  Best Local Similarity   100.0%;  Pred. No. 0;
  Matches 1132;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 MPRAPRCRAVRSLLRSHYREVLPLATFVRRLGPQGWRLVQRGDPAAFRALVAQCLVCVPW 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 MPRAPRCRAVRSLLRSHYREVLPLATFVRRLGPQGWRLVQRGDPAAFRALVAQCLVCVPW 60

Qy         61 DARPPPAAPSFRQVSCLKELVARVLQRLCERGAKNVLAFGFALLDGARGGPPEAFTTSVR 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 DARPPPAAPSFRQVSCLKELVARVLQRLCERGAKNVLAFGFALLDGARGGPPEAFTTSVR 120

Qy        121 SYLPNTVTDALRGSGAWGLLLRRVGDDVLVHLLARCALFVLVAPSCAYQVCGPPLYQLGA 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 SYLPNTVTDALRGSGAWGLLLRRVGDDVLVHLLARCALFVLVAPSCAYQVCGPPLYQLGA 180

Qy        181 ATQARPPPHASGPRRRLGCERAWNHSVREAGVPLGLPAPGARRRGGSASRSLPLPKRPRR 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 ATQARPPPHASGPRRRLGCERAWNHSVREAGVPLGLPAPGARRRGGSASRSLPLPKRPRR 240

Qy        241 GAAPEPERTPVGQGSWAHPGRTRGPSDRGFCVVSPARPAEEATSLEGALSGTRHSHPSVG 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 GAAPEPERTPVGQGSWAHPGRTRGPSDRGFCVVSPARPAEEATSLEGALSGTRHSHPSVG 300

Qy        301 RQHHAGPPSTSRPPRPWDTPCPPVYAETKHFLYSSGDKEQLRPSFLLSSLRPSLTGARRL 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 RQHHAGPPSTSRPPRPWDTPCPPVYAETKHFLYSSGDKEQLRPSFLLSSLRPSLTGARRL 360

Qy        361 VETIFLGSRPWMPGTPRRLPRLPQRYWQMRPLFLELLGNHAQCPYGVLLKTHCPLRAAVT 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        361 VETIFLGSRPWMPGTPRRLPRLPQRYWQMRPLFLELLGNHAQCPYGVLLKTHCPLRAAVT 420

Qy        421 PAAGVCAREKPQGSVAAPEEEDTDPRRLVQLLRQHSSPWQVYGFVRACLRRLVPPGLWGS 480
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        421 PAAGVCAREKPQGSVAAPEEEDTDPRRLVQLLRQHSSPWQVYGFVRACLRRLVPPGLWGS 480

Qy        481 RHNERRFLRNTKKFISLGKHAKLSLQELTWKMSVRDCAWLRRSPGVGCVPAAEHRLREEI 540
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        481 RHNERRFLRNTKKFISLGKHAKLSLQELTWKMSVRDCAWLRRSPGVGCVPAAEHRLREEI 540

Qy        541 LAKFLHWLMSVYVVELLRSFFYVTETTFQKNRLFFYRKSVWSKLQSIGIRQHLKRVQLRE 600
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        541 LAKFLHWLMSVYVVELLRSFFYVTETTFQKNRLFFYRKSVWSKLQSIGIRQHLKRVQLRE 600

Qy        601 LSEAEVRQHREARPALLTSRLRFIPKPDGLRPIVNMDYVVGARTFRREKRAERLTSRVKA 660
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        601 LSEAEVRQHREARPALLTSRLRFIPKPDGLRPIVNMDYVVGARTFRREKRAERLTSRVKA 660

Qy        661 LFSVLNYERARRPGLLGASVLGLDDIHRAWRTFVLRVRAQDPPPELYFVKVDVTGAYDTI 720
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        661 LFSVLNYERARRPGLLGASVLGLDDIHRAWRTFVLRVRAQDPPPELYFVKVDVTGAYDTI 720

Qy        721 PQDRLTEVIASIIKPQNTYCVRRYAVVQKAAHGHVRKAFKSHVSTLTDLQPYMRQFVAHL 780
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        721 PQDRLTEVIASIIKPQNTYCVRRYAVVQKAAHGHVRKAFKSHVSTLTDLQPYMRQFVAHL 780

Qy        781 QETSPLRDAVVIEQSSSLNEASSGLFDVFLRFMCHHAVRIRGKSYVQCQGIPQGSILSTL 840
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        781 QETSPLRDAVVIEQSSSLNEASSGLFDVFLRFMCHHAVRIRGKSYVQCQGIPQGSILSTL 840

Qy        841 LCSLCYGDMENKLFAGIRRDGLLLRLVDDFLLVTPHLTHAKTFLRTLVRGVPEYGCVVNL 900
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        841 LCSLCYGDMENKLFAGIRRDGLLLRLVDDFLLVTPHLTHAKTFLRTLVRGVPEYGCVVNL 900

Qy        901 RKTVVNFPVEDEALGGTAFVQMPAHGLFPWCGLLLDTRTLEVQSDYSSYARTSIRASLTF 960
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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```
Db        901 RKTVVNFPVEDEALGGTAFVQMPAHGLFPWCGLLLDTRTLEVQSDYSSYARTSIRASLTF 960

Qy        961 NRGFKAGRNMRRKLFGVLRLKCHSLFLDLQVNSLQTVCTNIYKILLLQAYRFHACVLQLP 1020
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        961 NRGFKAGRNMRRKLFGVLRLKCHSLFLDLQVNSLQTVCTNIYKILLLQAYRFHACVLQLP 1020

Qy       1021 FHQQVWKNPTFFLRVISDTASLCYSILKAKNAGMSLGAKGAAGPLPSEAVQWLCHQAFLL 1080
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1021 FHQQVWKNPTFFLRVISDTASLCYSILKAKNAGMSLGAKGAAGPLPSEAVQWLCHQAFLL 1080

Qy       1081 KLTRHRVTYVPLLGSLRTAQTQLSRKLPGTTLTALEAAANPALPSDFKTILD 1132
              |||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1081 KLTRHRVTYVPLLGSLRTAQTQLSRKLPGTTLTALEAAANPALPSDFKTILD 1132
```

RESULT 18
ADH72743
ID ADH72743 standard; protein; 1132 AA.
XX
AC ADH72743;
XX
DT 25-MAR-2004 (first entry)
XX
DE Human protein of the invention SEQ ID NO:19.
XX
KW stem cell; cardiant; hepatotropic; nephrotropic; cytostatic; nootropic;
KW neuroprotective; antiarthritic; antidiabetic; antiarteriosclerotic;
KW heart failure; leukaemia; neurodegenerative disease; diabetes;
KW arteriosclerosis; skeletal muscle; human.
XX
OS Homo sapiens.
XX
PN WO2003027281-A2.
XX
PD 03-APR-2003.
XX
PF 20-SEP-2002; 2002WO-JP009702.
XX
PR 20-SEP-2001; 2001JP-00286332.
PR 09-MAY-2002; 2002JP-00133575.
XX
PA (KYOW) KYOWA HAKKO KOGYO KK.
PA (TAMA/) TAMAKI T.
PA (ANDO/) ANDO K.
XX
PI Tamaki T, Ando K, Akatsuka A, Nakamura Y, Hotta T, Sakurada K;
XX
DR WPI; 2003-371925/35.
XX
PT Pluripotent stem cells originating in skeletal muscle interstitial
PT tissue, useful in drugs for regenerating tissues and cells e.g. in
PT treating heart failure, leukemia, neurodegenerative diseases, and
PT diabetes.
XX
PS Disclosure; SEQ ID NO 19; 29pp; Japanese.
XX
CC The invention relates to novel pluripotent stem cells originating from a
CC skeletal muscle interstitial tissue. A cell of the invention has
CC cardiant, hepatotropic, nephrotropic, cytostatic, nootropic,
CC neuroprotective, antiarthritic, antidiabetic, and antiarteriosclerotic
CC activity. The cells are useful in drugs for regenerating tissues and
CC cells e.g. in treating heart failure, leukaemia, neurodegenerative
CC diseases, diabetes and arteriosclerosis. The pluripotent stem cells were
CC isolated from rat skeletal muscles after analysis of the various
CC components by culturing and staining, as well as by other biochemical
CC analysis. The present sequence is used in the exemplification of the
CC invention.
XX
SQ Sequence 1132 AA;

Query Match 100.0%; Score 5961; DB 7; Length 1132;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1132; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy           1 MPRAPRCRAVRSLLRSHYREVLPLATFVRRLGPQGWRLVQRGDPAAFRALVAQCLVCVPW 60
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db           1 MPRAPRCRAVRSLLRSHYREVLPLATFVRRLGPQGWRLVQRGDPAAFRALVAQCLVCVPW 60

Qy          61 DARPPPAAPSFRQVSCLKELVARVLQRLCERGAKNVLAFGFALLDGARGGPPEAFTTSVR 120
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          61 DARPPPAAPSFRQVSCLKELVARVLQRLCERGAKNVLAFGFALLDGARGGPPEAFTTSVR 120

Qy         121 SYLPNTVTDALRGSGAWGLLLRRVGDDVLVHLLARCALFVLVAPSCAYQVCGPPLYQLGA 180
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         121 SYLPNTVTDALRGSGAWGLLLRRVGDDVLVHLLARCALFVLVAPSCAYQVCGPPLYQLGA 180

Qy         181 ATQARPPPHASGPRRRLGCERAWNHSVREAGVPLGLPAPGARRRGGSASRSLPLPKRPRR 240
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         181 ATQARPPPHASGPRRRLGCERAWNHSVREAGVPLGLPAPGARRRGGSASRSLPLPKRPRR 240

Qy         241 GAAPEPERTPVGQGSWAHPGRTRGPSDRGFCVVSPARPAEEATSLEGALSGTRHSHPSVG 300
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         241 GAAPEPERTPVGQGSWAHPGRTRGPSDRGFCVVSPARPAEEATSLEGALSGTRHSHPSVG 300

Qy         301 RQHHAGPPSTSRPPRPWDTPCPPVYAETKHFLYSSGDKEQLRPSFLLSSLRPSLTGARRL 360
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         301 RQHHAGPPSTSRPPRPWDTPCPPVYAETKHFLYSSGDKEQLRPSFLLSSLRPSLTGARRL 360

Qy         361 VETIFLGSRPWMPGTPRRLPRLPQRYWQMRPLFLELLGNHAQCPYGVLLKTHCPLRAAVT 420
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         361 VETIFLGSRPWMPGTPRRLPRLPQRYWQMRPLFLELLGNHAQCPYGVLLKTHCPLRAAVT 420

Qy         421 PAAGVCAREKPQGSVAAPEEEDTDPRRLVQLLRQHSSPWQVYGFVRACLRRLVPPGLWGS 480
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         421 PAAGVCAREKPQGSVAAPEEEDTDPRRLVQLLRQHSSPWQVYGFVRACLRRLVPPGLWGS 480

Qy         481 RHNERRFLRNTKKFISLGKHAKLSLQELTWKMSVRDCAWLRRSPGVGCVPAAEHRLREEI 540
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         481 RHNERRFLRNTKKFISLGKHAKLSLQELTWKMSVRDCAWLRRSPGVGCVPAAEHRLREEI 540

Qy         541 LAKFLHWLMSVYVVELLRSFFYVTETTFQKNRLFFYRKSVWSKLQSIGIRQHLKRVQLRE 600
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         541 LAKFLHWLMSVYVVELLRSFFYVTETTFQKNRLFFYRKSVWSKLQSIGIRQHLKRVQLRE 600

Qy         601 LSEAEVRQHREARPALLTSRLRFIPKPDGLRPIVNMDYVVGARTFRREKRAERLTSRVKA 660
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         601 LSEAEVRQHREARPALLTSRLRFIPKPDGLRPIVNMDYVVGARTFRREKRAERLTSRVKA 660

Qy         661 LFSVLNYERARRPGLLGASVLGLDDIHRAWRTFVLRVRAQDPPPELYFVKVDVTGAYDTI 720
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         661 LFSVLNYERARRPGLLGASVLGLDDIHRAWRTFVLRVRAQDPPPELYFVKVDVTGAYDTI 720

Qy         721 PQDRLTEVIASIIKPQNTYCVRRYAVVQKAAHGHVRKAFKSHVSTLTDLQPYMRQFVAHL 780
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         721 PQDRLTEVIASIIKPQNTYCVRRYAVVQKAAHGHVRKAFKSHVSTLTDLQPYMRQFVAHL 780

Qy         781 QETSPLRDAVVIEQSSSLNEASSGLFDVFLRFMCHHAVRIRGKSYVQCQGIPQGSILSTL 840
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         781 QETSPLRDAVVIEQSSSLNEASSGLFDVFLRFMCHHAVRIRGKSYVQCQGIPQGSILSTL 840

Qy         841 LCSLCYGDMENKLFAGIRRDGLLLRLVDDFLLVTPHLTHAKTFLRTLVRGVPEYGCVVNL 900
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         841 LCSLCYGDMENKLFAGIRRDGLLLRLVDDFLLVTPHLTHAKTFLRTLVRGVPEYGCVVNL 900

Qy         901 RKTVVNFPVEDEALGGTAFVQMPAHGLFPWCGLLLDTRTLEVQSDYSSYARTSIRASLTF 960
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         901 RKTVVNFPVEDEALGGTAFVQMPAHGLFPWCGLLLDTRTLEVQSDYSSYARTSIRASLTF 960

Qy         961 NRGFKAGRNMRRKLFGVLRLKCHSLFLDLQVNSLQTVCTNIYKILLLQAYRFHACVLQLP 1020
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         961 NRGFKAGRNMRRKLFGVLRLKCHSLFLDLQVNSLQTVCTNIYKILLLQAYRFHACVLQLP 1020

Qy        1021 FHQQVWKNPTFFLRVISDTASLCYSILKAKNAGMSLGAKGAAGPLPSEAVQWLCHQAFLL 1080
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        1021 FHQQVWKNPTFFLRVISDTASLCYSILKAKNAGMSLGAKGAAGPLPSEAVQWLCHQAFLL 1080
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```
Qy       1081 KLTRHRVTYVPLLGSLRTAQTQLSRKLPGTTLTALEAAANPALPSDFKTILD 1132
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1081 KLTRHRVTYVPLLGSLRTAQTQLSRKLPGTTLTALEAAANPALPSDFKTILD 1132


RESULT 19
ADG70114
ID   ADG70114 standard; protein; 1132 AA.
XX
AC   ADG70114;
XX
DT   11-MAR-2004  (first entry)
XX
DE   hTERT protein.
XX
KW   cytostatic; gene therapy; reverse transcriptase-Inhibitor; HIV-1;
KW   human telomerase reverse transcriptase; hTERT; chimeric; catalytic site;
KW   unregulated cellular growth; cancer; tumor.
XX
OS   Homo sapiens.
XX
PN   WO2003095605-A2.
XX
PD   20-NOV-2003.
XX
PF   14-APR-2003; 2003WO-EP003874.
XX
PR   08-MAY-2002; 2002US-0378820P.
XX
PA   (PHAA ) PHARMACIA ITAL SPA.
XX
PI   Moll J,  Schnuchel A,  Stouten P;
XX
DR   WPI; 2004-012095/01.
DR   N-PSDB; ADG70113.
XX
PT   New HIV-1 Reverse Transcriptase and human Telomerase Reverse
PT   Transcriptase proteins and nucleic acids, useful in gene therapy or for
PT   treating or preventing unregulated cellular growth, e.g. cancer cell or
PT   tumor growth.
XX
PS   Example 1; SEQ ID NO 4; 141pp; English.
XX
CC   The invention relates to the isolation of compounds that bind and inhibit
CC   the activity of HIV-1 reverse transcriptase (RT) or human telomerase
CC   reverse transcriptase (hTERT). The method involves determining these
CC   compounds using a HIV-1 RT/hTERT chimeric construct containing the
CC   catalytic sites of each enzyme. The nucleic acid is useful for treating
CC   or preventing unregulated cellular growth, including cancer cell and
CC   tumor growth. It is also useful in gene therapy. Compounds that inhibit
CC   telomerase activity can be used to treat cancer. The vectors of the
CC   invention can be used to amplify DNA or RNA encoding HIV-RT/hTERT and/or
CC   express DNA which encodes HIV-RT/hTERT. This sequence corresponds to the
CC   human TERT protein.
XX
SQ   Sequence 1132 AA;

  Query Match           100.0%;  Score 5961;  DB 8;  Length 1132;
  Best Local Similarity  100.0%;  Pred. No. 0;
  Matches 1132;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 MPRAPRCRAVRSLLRSHYREVLPLATFVRRLGPQGWRLVQRGDPAAFRALVAQCLVCVPW 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 MPRAPRCRAVRSLLRSHYREVLPLATFVRRLGPQGWRLVQRGDPAAFRALVAQCLVCVPW 60

Qy         61 DARPPPAAPSFRQVSCLKELVARVLQRLCERGAKNVLAFGFALLDGARGGPPEAFTTSVR 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 DARPPPAAPSFRQVSCLKELVARVLQRLCERGAKNVLAFGFALLDGARGGPPEAFTTSVR 120

Qy        121 SYLPNTVTDALRGSGAWGLLLRRVGDDVLVHLLARCALFVLVAPSCAYQVCGPPLYQLGA 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 SYLPNTVTDALRGSGAWGLLLRRVGDDVLVHLLARCALFVLVAPSCAYQVCGPPLYQLGA 180

Qy        181 ATQARPPPHASGPRRRLGCERAWNHSVREAGVPLGLPAPGARRRGGSASRSLPLPKRPRR 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 ATQARPPPHASGPRRRLGCERAWNHSVREAGVPLGLPAPGARRRGGSASRSLPLPKRPRR 240

Qy        241 GAAPEPERTPVGQGSWAHPGRTRGPSDRGFCVVSPARPAEEATSLEGALSGTRHSHPSVG 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 GAAPEPERTPVGQGSWAHPGRTRGPSDRGFCVVSPARPAEEATSLEGALSGTRHSHPSVG 300

Qy        301 RQHHAGPPSTSRPPRPWDTPCPPVYAETKHFLYSSGDKEQLRPSFLLSSLRPSLTGARRL 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 RQHHAGPPSTSRPPRPWDTPCPPVYAETKHFLYSSGDKEQLRPSFLLSSLRPSLTGARRL 360

Qy        361 VETIFLGSRPWMPGTPRRLPRLPQRYWQMRPLFLELLGNHAQCPYGVLLKTHCPLRAAVT 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        361 VETIFLGSRPWMPGTPRRLPRLPQRYWQMRPLFLELLGNHAQCPYGVLLKTHCPLRAAVT 420

Qy        421 PAAGVCAREKPQGSVAAPEEEDTDPRRLVQLLRQHSSPWQVYGFVRACLRRLVPPGLWGS 480
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        421 PAAGVCAREKPQGSVAAPEEEDTDPRRLVQLLRQHSSPWQVYGFVRACLRRLVPPGLWGS 480

Qy        481 RHNERRFLRNTKKFISLGKHAKLSLQELTWKMSVRDCAWLRRSPGVGCVPAAEHRLREEI 540
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        481 RHNERRFLRNTKKFISLGKHAKLSLQELTWKMSVRDCAWLRRSPGVGCVPAAEHRLREEI 540

Qy        541 LAKFLHWLMSVYVVELLRSFFYVTETTFQKNRLFFYRKSVWSKLQSIGIRQHLKRVQLRE 600
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        541 LAKFLHWLMSVYVVELLRSFFYVTETTFQKNRLFFYRKSVWSKLQSIGIRQHLKRVQLRE 600

Qy        601 LSEAEVRQHREARPALLTSRLRFIPKPDGLRPIVNMDYVVGARTFRREKRAERLTSRVKA 660
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        601 LSEAEVRQHREARPALLTSRLRFIPKPDGLRPIVNMDYVVGARTFRREKRAERLTSRVKA 660

Qy        661 LFSVLNYERARRPGLLGASVLGLDDIHRAWRTFVLRVRAQDPPPELYFVKVDVTGAYDTI 720
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        661 LFSVLNYERARRPGLLGASVLGLDDIHRAWRTFVLRVRAQDPPPELYFVKVDVTGAYDTI 720

Qy        721 PQDRLTEVIASIIKPQNTYCVRRYAVVQKAAHGHVRKAFKSHVSTLTDLQPYMRQFVAHL 780
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        721 PQDRLTEVIASIIKPQNTYCVRRYAVVQKAAHGHVRKAFKSHVSTLTDLQPYMRQFVAHL 780

Qy        781 QETSPLRDAVVIEQSSSLNEASSGLFDVFLRFMCHHAVRIRGKSYVQCQGIPQGSILSTL 840
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        781 QETSPLRDAVVIEQSSSLNEASSGLFDVFLRFMCHHAVRIRGKSYVQCQGIPQGSILSTL 840

Qy        841 LCSLCYGDMENKLFAGIRRDGLLLRLVDDFLLVTPHLTHAKTFLRTLVRGVPEYGCVVNL 900
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        841 LCSLCYGDMENKLFAGIRRDGLLLRLVDDFLLVTPHLTHAKTFLRTLVRGVPEYGCVVNL 900

Qy        901 RKTVVNFPVEDEALGGTAFVQMPAHGLFPWCGLLLDTRTLEVQSDYSSYARTSIRASLTF 960
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        901 RKTVVNFPVEDEALGGTAFVQMPAHGLFPWCGLLLDTRTLEVQSDYSSYARTSIRASLTF 960

Qy        961 NRGFKAGRNMRRKLFGVLRLKCHSLFLDLQVNSLQTVCTNIYKILLLQAYRFHACVLQLP 1020
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        961 NRGFKAGRNMRRKLFGVLRLKCHSLFLDLQVNSLQTVCTNIYKILLLQAYRFHACVLQLP 1020

Qy       1021 FHQQVWKNPTFFLRVISDTASLCYSILKAKNAGMSLGAKGAAGPLPSEAVQWLCHQAFLL 1080
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1021 FHQQVWKNPTFFLRVISDTASLCYSILKAKNAGMSLGAKGAAGPLPSEAVQWLCHQAFLL 1080

Qy       1081 KLTRHRVTYVPLLGSLRTAQTQLSRKLPGTTLTALEAAANPALPSDFKTILD 1132
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1081 KLTRHRVTYVPLLGSLRTAQTQLSRKLPGTTLTALEAAANPALPSDFKTILD 1132


RESULT 20
ADG90599
ID   ADG90599 standard; protein; 1132 AA.
XX
AC   ADG90599;
XX
DT   25-MAR-2004  (first entry)
XX
```

DE Human TERT SEQ ID NO:2.
XX
KW human; immune response; telomerase reverse transcriptase; TERT;
KW cytostatic; immunostimulant; cancer; cytotoxic T cell response.
XX
OS Homo sapiens.
XX
PN WO2004002408-A2.
XX
PD 08-JAN-2004.
XX
PF 24-JUN-2003; 2003WO-US019844.
XX
PR 27-JUN-2002; 2002US-0393295P.
XX
PA (GERO-) GERON CORP.
XX
PI Majumdar A, Ferber IA, Frolkis M, Wang Z;
XX
DR WPI; 2004-071946/07.
DR N-PSDB; ADG90598.
XX
PT Eliciting an immune response in a mammal specific for its own telomerase
PT reverse transcriptase (TERT), useful for treating or preventing cancer,
PT comprises administering a composition containing TERT of another
PT mammalian species.
XX
PS Claim 66; SEQ ID NO 2; 44pp; English.
XX
CC The invention relates to a novel method for eliciting an immune response
CC in a mammalian subject that is specific for its own telomerase reverse
CC transcriptase (TERT), comprising administering an immunogenic composition
CC containing a protein with at least 20 consecutive amino acids of TERT of
CC another mammalian species, or a nucleic acid encoding the protein. A
CC composition of the invention has cytostatic, and immunostimulant
CC activity. The protein or the nucleic acid encoding the protein is useful
CC in the manufacture of a medicament for the treatment of cancer in a human
CC or for eliciting a cytotoxic T cell response in a human.
XX
SQ Sequence 1132 AA;

Query Match 100.0%; Score 5961; DB 8; Length 1132;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1132; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```
Qy          1 MPRAPRCRAVRSLLRSHYREVLPLATFVRRLGPQGWRLVQRGDPAAFRALVAQCLVCVPW 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 MPRAPRCRAVRSLLRSHYREVLPLATFVRRLGPQGWRLVQRGDPAAFRALVAQCLVCVPW 60

Qy         61 DARPPPAAPSFRQVSCLKELVARVLQRLCERGAKNVLAFGFALLDGARGGPPEAFTTSVR 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 DARPPPAAPSFRQVSCLKELVARVLQRLCERGAKNVLAFGFALLDGARGGPPEAFTTSVR 120

Qy        121 SYLPNTVTDALRGSGAWGLLLRRVGDDVLVHLLARCALFVLVAPSCAYQVCGPPLYQLGA 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 SYLPNTVTDALRGSGAWGLLLRRVGDDVLVHLLARCALFVLVAPSCAYQVCGPPLYQLGA 180

Qy        181 ATQARPPPHASGPRRRLGCERAWNHSVREAGVPLGLPAPGARRRGGSASRSLPLPKRPRR 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 ATQARPPPHASGPRRRLGCERAWNHSVREAGVPLGLPAPGARRRGGSASRSLPLPKRPRR 240

Qy        241 GAAPEPERTPVGQGSWAHPGRTRGPSDRGFCVVSPARPAEEATSLEGALSGTRHSHPSVG 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 GAAPEPERTPVGQGSWAHPGRTRGPSDRGFCVVSPARPAEEATSLEGALSGTRHSHPSVG 300

Qy        301 RQHHAGPPSTSRPPRPWDTPCPPVYAETKHFLYSSGDKEQLRPSFLLSSLRPSLTGARRL 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 RQHHAGPPSTSRPPRPWDTPCPPVYAETKHFLYSSGDKEQLRPSFLLSSLRPSLTGARRL 360

Qy        361 VETIFLGSRPWMPGTPRRLPRLPQRYWQMRPLFLELLGNHAQCPYGVLLKTHCPLRAAVT 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        361 VETIFLGSRPWMPGTPRRLPRLPQRYWQMRPLFLELLGNHAQCPYGVLLKTHCPLRAAVT 420

Qy        421 PAAGVCAREKPQGSVAAPEEEDTDPRRLVQLLRQHSSPWQVYGFVRACLRRLVPPGLWGS 480
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        421 PAAGVCAREKPQGSVAAPEEEDTDPRRLVQLLRQHSSPWQVYGFVRACLRRLVPPGLWGS 480

Qy        481 RHNERRFLRNTKKFISLGKHAKLSLQELTWKMSVRDCAWLRRSPGVGCVPAAEHRLREEI 540
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        481 RHNERRFLRNTKKFISLGKHAKLSLQELTWKMSVRDCAWLRRSPGVGCVPAAEHRLREEI 540

Qy        541 LAKFLHWLMSVYVVELLRSFFYVTETTFQKNRLFFYRKSVWSKLQSIGIRQHLKRVQLRE 600
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        541 LAKFLHWLMSVYVVELLRSFFYVTETTFQKNRLFFYRKSVWSKLQSIGIRQHLKRVQLRE 600

Qy        601 LSEAEVRQHREARPALLTSRLRFIPKPDGLRPIVNMDYVVGARTFRREKRAERLTSRVKA 660
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        601 LSEAEVRQHREARPALLTSRLRFIPKPDGLRPIVNMDYVVGARTFRREKRAERLTSRVKA 660

Qy        661 LFSVLNYERARRPGLLGASVLGLDDIHRAWRTFVLRVRAQDPPPELYFVKVDVTGAYDTI 720
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        661 LFSVLNYERARRPGLLGASVLGLDDIHRAWRTFVLRVRAQDPPPELYFVKVDVTGAYDTI 720

Qy        721 PQDRLTEVIASIIKPQNTYCVRRYAVVQKAAHGHVRKAFKSHVSTLTDLQPYMRQFVAHL 780
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        721 PQDRLTEVIASIIKPQNTYCVRRYAVVQKAAHGHVRKAFKSHVSTLTDLQPYMRQFVAHL 780

Qy        781 QETSPLRDAVVIEQSSSLNEASSGLFDVFLRFMCHHAVRIRGKSYVQCQGIPQGSILSTL 840
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        781 QETSPLRDAVVIEQSSSLNEASSGLFDVFLRFMCHHAVRIRGKSYVQCQGIPQGSILSTL 840

Qy        841 LCSLCYGDMENKLFAGIRRDGLLLRLVDDFLLVTPHLTHAKTFLRTLVRGVPEYGCVVNL 900
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        841 LCSLCYGDMENKLFAGIRRDGLLLRLVDDFLLVTPHLTHAKTFLRTLVRGVPEYGCVVNL 900

Qy        901 RKTVVNFPVEDEALGGTAFVQMPAHGLFPWCGLLLDTRTLEVQSDYSSYARTSIRASLTF 960
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        901 RKTVVNFPVEDEALGGTAFVQMPAHGLFPWCGLLLDTRTLEVQSDYSSYARTSIRASLTF 960

Qy        961 NRGFKAGRNMRRKLFGVLRLKCHSLFLDLQVNSLQTVCTNIYKILLLQAYRFHACVLQLP 1020
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        961 NRGFKAGRNMRRKLFGVLRLKCHSLFLDLQVNSLQTVCTNIYKILLLQAYRFHACVLQLP 1020

Qy       1021 FHQQVWKNPTFFLRVISDTASLCYSILKAKNAGMSLGAKGAAGPLPSEAVQWLCHQAFLL 1080
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1021 FHQQVWKNPTFFLRVISDTASLCYSILKAKNAGMSLGAKGAAGPLPSEAVQWLCHQAFLL 1080

Qy       1081 KLTRHRVTYVPLLGSLRTAQTQLSRKLPGTTLTALEAAANPALPSDFKTILD 1132
              |||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1081 KLTRHRVTYVPLLGSLRTAQTQLSRKLPGTTLTALEAAANPALPSDFKTILD 1132
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RESULT 21
ADI82172
ID ADI82172 standard; protein; 1132 AA.
XX
AC ADI82172;
XX
DT 22-APR-2004 (first entry)
XX
DE Human telomerase reverse transcriptase.
XX
KW Human; embryonic stem cell; pluripotent stem cell; abnormal cell growth;
KW malignancy; differentiation.
XX
OS Homo sapiens.
XX
PN US2003224411-A1.
XX
PD 04-DEC-2003.
XX
PF 13-MAR-2003; 2003US-00388578.
XX
PR 13-MAR-2003; 2003US-00388578.
XX
PA (STAN/) STANTON L W.

PA (BRAN/) BRANDENBERGER R.
PA (GOLD/) GOLD J D.
PA (IRVI/) IRVING J M.
PA (MAND/) MANDALAM R.
PA (MOKM/) MOK M.
PA (SHEL/) SHELTON D.
XX
PI Stanton LW, Brandenberger R, Gold JD, Irving JM, Mandalam R;
PI Mok M, Shelton D;
XX
DR WPI; 2004-119701/12.
DR N-PSDB; ADI82171.
XX
PT Assessing culture of undifferentiated primate pluripotent stem cells by
PT detecting expression of markers e.g., Zic family member 3, other than
PT human telomerase reverse transcriptase/octamer binding transcription
PT factor.
XX
PS Claim 1; SEQ ID NO 2; 106pp; English.
XX
CC The invention relates to assessing a culture of undifferentiated primate
CC pluripotent stem cells (pPS, e.g. embryonic stem cells), involving
CC detecting expression of markers (MR1) e.g. Zic family member 3 (ZIC3), as
CC given in specification, other than human telomerase reverse transcriptase
CC (hTERT) or octamer binding transcription factor (Oct)3/4, or a marker
CC (MR2) such as cripto or podocalyxin-like protein and hTERT and/or Oct3/4
CC or second marker chosen from (MR2). Also included are maintaining (M2)
CC pPS cells in a pluripotent state (involves causing them to express one of
CC the following markers (MR3) at a higher level, FOXO1A, ZIC3, hypothetical
CC protein FLJ20582, Forkhead box H1 (FOXH1), Zinc finger protein, Hsal2,
CC KRAB-zinc finger protein SZF1-1 or zinc finger protein of cerebellum
CC ZIC2, or any other marker (MR4) chosen from PHD protein Jade-1 (Jade-1),
CC kruppel-like zinc finger protein (ZNF300), etc., as given in the
CC specification), causing pPS cells to differentiate into a particular
CC tissue type by causing them to express one of the markers chosen from
CC (MR3) or (MR4)(or markers chosen from GATA binding protein 3 (GATA3),
CC core promoter element binding protein (COPEB), etc., as given in the
CC specification), maintaining pPS cells in a pluripotent state (involves
CC culturing pPS cells or their progeny in the presence of a normally
CC secreted protein that is encoded by a gene that down-regulated upon
CC differentiation of human embryonic stem (hES) cells, chosen from
CC Fibrillin 3 gene, LEFT B gene, ZIC3 gene, EPHA1 gene, etc., as given in
CC the specification), causing pPS cells to differentiate (involves
CC culturing pPS cells or their progeny in the presence of a normally
CC secreted protein that is encoded by a gene that up-regulated upon
CC differentiation of hES cells, chosen from P311 protein gene, Tax
CC interaction protein 1 gene, KIAA0853 protein gene, keratin 19 (KRT 19)
CC gene, etc., as given in the specification), causing an encoding sequence
CC to be preferentially expressed in undifferentiated pPS cells, causing an
CC encoding sequence to be preferentially expressed in differentiated cells,
CC sorting (M4) differentiated cells from less differentiated cells
CC (involves separating cells expressing a surface marker chosen from any
CC one of MR1 from cells not expressing the marker), causing pPS cells to
CC proliferate without differentiation, identifying genes that are up or
CC down regulated during differentiation of pPS cells, and a kit (I) for
CC assessing a culture of pPS cells by M1. The method (M1) is useful for
CC assessing culture of undifferentiated primate pluripotent stem cells and
CC for assessing the growth characteristics of a cell population. The cell
CC population has been obtained by culturing cells from human blastocyst or
CC from a human patient suspected of having a clinical condition related to
CC abnormal cell growth. The method further involves determining whether the
CC cell population is pluripotent from the marker expression and assessing
CC whether the patient has a malignancy from the marker expression. The
CC present sequence is a protein whose expression is down regulated in
CC pluripotent stem cells.
XX
SQ Sequence 1132 AA;

Query Match 100.0%; Score 5961; DB 8; Length 1132;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1132; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy          1 MPRAPRCRAVRSLLRSHYREVLPLATFVRRLGPQGWRLVQRGDPAAFRALVAQCLVCVPW 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 MPRAPRCRAVRSLLRSHYREVLPLATFVRRLGPQGWRLVQRGDPAAFRALVAQCLVCVPW 60

Qy         61 DARPPPAAPSFRQVSCLKELVARVLQRLCERGAKNVLAFGFALLDGARGGPPEAFTTSVR 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 DARPPPAAPSFRQVSCLKELVARVLQRLCERGAKNVLAFGFALLDGARGGPPEAFTTSVR 120

Qy        121 SYLPNTVTDALRGSGAWGLLLRRVGDDVLVHLLARCALFVLVAPSCAYQVCGPPLYQLGA 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 SYLPNTVTDALRGSGAWGLLLRRVGDDVLVHLLARCALFVLVAPSCAYQVCGPPLYQLGA 180

Qy        181 ATQARPPPHASGPRRRLGCERAWNHSVREAGVPLGLPAPGARRRGGSASRSLPLPKRPRR 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 ATQARPPPHASGPRRRLGCERAWNHSVREAGVPLGLPAPGARRRGGSASRSLPLPKRPRR 240

Qy        241 GAAPEPERTPVGQGSWAHPGRTRGPSDRGFCVVSPARPAEEATSLEGALSGTRHSHPSVG 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 GAAPEPERTPVGQGSWAHPGRTRGPSDRGFCVVSPARPAEEATSLEGALSGTRHSHPSVG 300

Qy        301 RQHHAGPPSTSRPPRPWDTPCPPVYAETKHFLYSSGDKEQLRPSFLLSSLRPSLTGARRL 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 RQHHAGPPSTSRPPRPWDTPCPPVYAETKHFLYSSGDKEQLRPSFLLSSLRPSLTGARRL 360

Qy        361 VETIFLGSRPWMPGTPRRLPRLPQRYWQMRPLFLELLGNHAQCPYGVLLKTHCPLRAAVT 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        361 VETIFLGSRPWMPGTPRRLPRLPQRYWQMRPLFLELLGNHAQCPYGVLLKTHCPLRAAVT 420

Qy        421 PAAGVCAREKPQGSVAAPEEEDTDPRRLVQLLRQHSSPWQVYGFVRACLRRLVPPGLWGS 480
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        421 PAAGVCAREKPQGSVAAPEEEDTDPRRLVQLLRQHSSPWQVYGFVRACLRRLVPPGLWGS 480

Qy        481 RHNERRFLRNTKKFISLGKHAKLSLQELTWKMSVRDCAWLRRSPGVGCVPAAEHRLREEI 540
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        481 RHNERRFLRNTKKFISLGKHAKLSLQELTWKMSVRDCAWLRRSPGVGCVPAAEHRLREEI 540

Qy        541 LAKFLHWLMSVYVVELLRSFFYVTETTFQKNRLFFYRKSVWSKLQSIGIRQHLKRVQLRE 600
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        541 LAKFLHWLMSVYVVELLRSFFYVTETTFQKNRLFFYRKSVWSKLQSIGIRQHLKRVQLRE 600

Qy        601 LSEAEVRQHREARPALLTSRLRFIPKPDGLRPIVNMDYVVGARTFRREKRAERLTSRVKA 660
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        601 LSEAEVRQHREARPALLTSRLRFIPKPDGLRPIVNMDYVVGARTFRREKRAERLTSRVKA 660

Qy        661 LFSVLNYERARRPGLLGASVLGLDDIHRAWRTFVLRVRAQDPPPELYFVKVDVTGAYDTI 720
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        661 LFSVLNYERARRPGLLGASVLGLDDIHRAWRTFVLRVRAQDPPPELYFVKVDVTGAYDTI 720

Qy        721 PQDRLTEVIASIIKPQNTYCVRRYAVVQKAAHGHVRKAFKSHVSTLTDLQPYMRQFVAHL 780
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        721 PQDRLTEVIASIIKPQNTYCVRRYAVVQKAAHGHVRKAFKSHVSTLTDLQPYMRQFVAHL 780

Qy        781 QETSPLRDAVVIEQSSSLNEASSGLFDVFLRFMCHHAVRIRGKSYVQCQGIPQGSILSTL 840
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        781 QETSPLRDAVVIEQSSSLNEASSGLFDVFLRFMCHHAVRIRGKSYVQCQGIPQGSILSTL 840

Qy        841 LCSLCYGDMENKLFAGIRRDGLLLRLVDDFLLVTPHLTHAKTFLRTLVRGVPEYGCVVNL 900
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        841 LCSLCYGDMENKLFAGIRRDGLLLRLVDDFLLVTPHLTHAKTFLRTLVRGVPEYGCVVNL 900

Qy        901 RKTVVNFPVEDEALGGTAFVQMPAHGLFPWCGLLLDTRTLEVQSDYSSYARTSIRASLTF 960
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        901 RKTVVNFPVEDEALGGTAFVQMPAHGLFPWCGLLLDTRTLEVQSDYSSYARTSIRASLTF 960

Qy        961 NRGFKAGRNMRRKLFGVLRLKCHSLFLDLQVNSLQTVCTNIYKILLLQAYRFHACVLQLP 1020
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        961 NRGFKAGRNMRRKLFGVLRLKCHSLFLDLQVNSLQTVCTNIYKILLLQAYRFHACVLQLP 1020

Qy       1021 FHQQVWKNPTFFLRVISDTASLCYSILKAKNAGMSLGAKGAAGPLPSEAVQWLCHQAFLL 1080
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1021 FHQQVWKNPTFFLRVISDTASLCYSILKAKNAGMSLGAKGAAGPLPSEAVQWLCHQAFLL 1080

Qy       1081 KLTRHRVTYVPLLGSLRTAQTQLSRKLPGTTLTALEAAANPALPSDFKTILD 1132
              ||||||||||||||||||||||||||||||||||||||||||||||||||||
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Db       1081 KLTRHRVTYVPLLGSLRTAQTQLSRKLPGTTLTALEAAANPALPSDFKTILD 1132


RESULT 22
AAW61350
ID   AAW61350 standard; protein; 1154 AA.
XX
AC   AAW61350;
XX
DT   25-MAR-2003  (revised)
DT   12-OCT-1998  (first entry)
XX
DE   Human telomerase protein 2 (TP2).
XX
KW   TP2; human; telomerase protein 2; cancer; AIDS; ageing; therapy.
XX
OS   Homo sapiens.
XX
PN   WO9821343-A1.
XX
PD   22-MAY-1998.
XX
PF   13-NOV-1997;   97WO-US021248.
XX
PR   15-NOV-1996;   96US-00751189.
PR   11-JUN-1997;   97US-00873039.
PR   16-OCT-1997;   97US-00951733.
XX
PA   (AMGE-) AMGEN INC.
PA   (AMGE-) AMGEN CANADA INC.
XX
PI   Harrington LA,  Robinson MO;
XX
DR   WPI; 1998-297946/26.
DR   N-PSDB; AAV27876.
XX
PT   New nucleic acid encoding human telomerase protein-2 - used for
PT   regulating telomerase activity, e.g. for treating cancer or acquired
PT   immune deficiency syndrome.
XX
PS   Claim 1e; Fig 9; 150pp; English.
XX
CC   This polypeptide comprises human telomerase protein 2 (TP2), a novel
CC   protein of the telomerase complex. Its amino acid sequence was deduced
CC   from a composite (see AAV27876) of isolated cDNA clones 32 (see AAV27872)
CC   and TP2-15 (see AAV27875), obtained from a human colon tumour cell line
CC   LIM1863 cDNA. Expressing TP2 in a cell is used to increase telomerase
CC   activity and thus proliferation for treatment of e.g. HIV infection, AIDS
CC   and ageing disorders, while expressing an inactive mutant of TP2 (or
CC   molecule antisense to the gene) is used to decrease telomerase activity,
CC   e.g. for treatment of cancer. TR2 polypeptides can also be used to screen
CC   for agents that inhibit TP2 activity or its binding to TRIP1 (see
CC   AAW61347) or telomerase RNA, potentially useful therapeutically, also to
CC   raise specific antibodies useful in immunoassays and therapeutically as
CC   inhibitors. Also contemplated are transgenic animals in which the TP2
CC   gene has been inactivated or is overexpressed. TP2 polypeptides are
CC   administered i.v., s.c. or orally, or they are delivered from engineered
CC   cells or gene therapy vectors. (Updated on 25-MAR-2003 to correct PR
CC   field.)
XX
SQ   Sequence 1154 AA;

  Query Match           100.0%;  Score 5961;  DB 2;  Length 1154;
  Best Local Similarity  100.0%;  Pred. No. 0;
  Matches 1132;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 MPRAPRCRAVRSLLRSHYREVLPLATFVRRLGPQGWRLVQRGDPAAFRALVAQCLVCVPW 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         23 MPRAPRCRAVRSLLRSHYREVLPLATFVRRLGPQGWRLVQRGDPAAFRALVAQCLVCVPW 82

Qy         61 DARPPPAAPSFRQVSCLKELVARVLQRLCERGAKNVLAFGFALLDGARGGPPEAFTTSVR 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         83 DARPPPAAPSFRQVSCLKELVARVLQRLCERGAKNVLAFGFALLDGARGGPPEAFTTSVR 142

Qy        121 SYLPNTVTDALRGSGAWGLLLRRVGDDVLVHLLARCALFVLVAPSCAYQVCGPPLYQLGA 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        143 SYLPNTVTDALRGSGAWGLLLRRVGDDVLVHLLARCALFVLVAPSCAYQVCGPPLYQLGA 202

Qy        181 ATQARPPPHASGPRRRLGCERAWNHSVREAGVPLGLPAPGARRRGGSASRSLPLPKRPRR 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        203 ATQARPPPHASGPRRRLGCERAWNHSVREAGVPLGLPAPGARRRGGSASRSLPLPKRPRR 262

Qy        241 GAAPEPERTPVGQGSWAHPGRTRGPSDRGFCVVSPARPAEEATSLEGALSGTRHSHPSVG 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        263 GAAPEPERTPVGQGSWAHPGRTRGPSDRGFCVVSPARPAEEATSLEGALSGTRHSHPSVG 322

Qy        301 RQHHAGPPSTSRPPRPWDTPCPPVYAETKHFLYSSGDKEQLRPSFLLSSLRPSLTGARRL 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        323 RQHHAGPPSTSRPPRPWDTPCPPVYAETKHFLYSSGDKEQLRPSFLLSSLRPSLTGARRL 382

Qy        361 VETIFLGSRPWMPGTPRRLPRLPQRYWQMRPLFLELLGNHAQCPYGVLLKTHCPLRAAVT 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        383 VETIFLGSRPWMPGTPRRLPRLPQRYWQMRPLFLELLGNHAQCPYGVLLKTHCPLRAAVT 442

Qy        421 PAAGVCAREKPQGSVAAPEEEDTDPRRLVQLLRQHSSPWQVYGFVRACLRRLVPPGLWGS 480
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        443 PAAGVCAREKPQGSVAAPEEEDTDPRRLVQLLRQHSSPWQVYGFVRACLRRLVPPGLWGS 502

Qy        481 RHNERRFLRNTKKFISLGKHAKLSLQELTWKMSVRDCAWLRRSPGVGCVPAAEHRLREEI 540
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        503 RHNERRFLRNTKKFISLGKHAKLSLQELTWKMSVRDCAWLRRSPGVGCVPAAEHRLREEI 562

Qy        541 LAKFLHWLMSVYVVELLRSFFYVTETTFQKNRLFFYRKSVWSKLQSIGIRQHLKRVQLRE 600
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        563 LAKFLHWLMSVYVVELLRSFFYVTETTFQKNRLFFYRKSVWSKLQSIGIRQHLKRVQLRE 622

Qy        601 LSEAEVRQHREARPALLTSRLRFIPKPDGLRPIVNMDYVVGARTFRREKRAERLTSRVKA 660
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        623 LSEAEVRQHREARPALLTSRLRFIPKPDGLRPIVNMDYVVGARTFRREKRAERLTSRVKA 682

Qy        661 LFSVLNYERARRPGLLGASVLGLDDIHRAWRTFVLRVRAQDPPPELYFVKVDVTGAYDTI 720
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        683 LFSVLNYERARRPGLLGASVLGLDDIHRAWRTFVLRVRAQDPPPELYFVKVDVTGAYDTI 742

Qy        721 PQDRLTEVIASIIKPQNTYCVRRYAVVQKAAHGHVRKAFKSHVSTLTDLQPYMRQFVAHL 780
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        743 PQDRLTEVIASIIKPQNTYCVRRYAVVQKAAHGHVRKAFKSHVSTLTDLQPYMRQFVAHL 802

Qy        781 QETSPLRDAVVIEQSSSLNEASSGLFDVFLRFMCHHAVRIRGKSYVQCQGIPQGSILSTL 840
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        803 QETSPLRDAVVIEQSSSLNEASSGLFDVFLRFMCHHAVRIRGKSYVQCQGIPQGSILSTL 862

Qy        841 LCSLCYGDMENKLFAGIRRDGLLLRLVDDFLLVTPHLTHAKTFLRTLVRGVPEYGCVVNL 900
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        863 LCSLCYGDMENKLFAGIRRDGLLLRLVDDFLLVTPHLTHAKTFLRTLVRGVPEYGCVVNL 922

Qy        901 RKTVVNFPVEDEALGGTAFVQMPAHGLFPWCGLLLDTRTLEVQSDYSSYARTSIRASLTF 960
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        923 RKTVVNFPVEDEALGGTAFVQMPAHGLFPWCGLLLDTRTLEVQSDYSSYARTSIRASLTF 982

Qy        961 NRGFKAGRNMRRKLFGVLRLKCHSLFLDLQVNSLQTVCTNIYKILLLQAYRFHACVLQLP 1020
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        983 NRGFKAGRNMRRKLFGVLRLKCHSLFLDLQVNSLQTVCTNIYKILLLQAYRFHACVLQLP 1042

Qy       1021 FHQQVWKNPTFFLRVISDTASLCYSILKAKNAGMSLGAKGAAGPLPSEAVQWLCHQAFLL 1080
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1043 FHQQVWKNPTFFLRVISDTASLCYSILKAKNAGMSLGAKGAAGPLPSEAVQWLCHQAFLL 1102

Qy       1081 KLTRHRVTYVPLLGSLRTAQTQLSRKLPGTTLTALEAAANPALPSDFKTILD 1132
              ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1103 KLTRHRVTYVPLLGSLRTAQTQLSRKLPGTTLTALEAAANPALPSDFKTILD 1154


RESULT 23
AAW47008
ID   AAW47008 standard; protein; 1189 AA.
```

```
XX
AC   AAW47008;
XX
DT   13-AUG-1998  (first entry)
XX
DE   Glutathione-S-transferase and hTRT fusion protein 8.
XX
KW   Human; telomerase reverse transcriptase; hTRT; TRT; diagnosis; prognosis;
KW   cell proliferation; cancer; ageing; ribonucleoprotein.
XX
OS   Synthetic.
OS   Homo sapiens.
XX
FH   Key             Location/Qualifiers
FT   Misc-difference 22. .23
FT                   /note= "enterokinase cleavage site"
XX
PN   GB2317891-A.
XX
PD   08-APR-1998.
XX
PF   01-OCT-1997;   97GB-00020890.
XX
PR   01-OCT-1996;   96US-00724643.
PR   18-APR-1997;   97US-00844419.
PR   25-APR-1997;   97US-00846017.
PR   06-MAY-1997;   97US-00851843.
PR   09-MAY-1997;   97US-00854050.
PR   14-AUG-1997;   97US-00911312.
PR   14-AUG-1997;   97US-00912951.
PR   14-AUG-1997;   97US-00915503.
XX
PA   (GERO-) GERON CORP.
PA   (UYTE-) UNIV TECHNOLOGY CORP.
XX
PI   Cech TR,  Lingner J,  Nakamura T,  Chapman KB,  Morin GB,  Harley CB;
PI   Andrews WH;
XX
DR   WPI; 1998-171633/16.
XX
PT   Pure and recombinant human Telomerase Reverse Transcriptase and its
PT   variants - are useful in the diagnosis, prognosis and treatment of cell
PT   proliferation conditions especially cancer and ageing.
XX
PS   Example 6; Page 234-235; 387pp; English.
XX
CC   The present sequence represents a fusion protein from an example of the
CC   present invention which describes human telomerase reverse transcriptase
CC   (hTRT). The present invention also describes the following methods: (A)
CC   determining whether a test compound is a modulator of hTRT, by detecting
CC   the change in hTRT recombinant protein or polynucleotide, on
CC   administration of the compound; (B) preparation of recombinant telomerase
CC   by contacting a protein preparation of hTRT with a telomerase RNA
CC   component; (C) detection of the hTRT RNA or protein in a sample by
CC   binding a relevant probe to the sample and detecting the complex formed
CC   or in the case of RNA detection, amplifying the product and correlating
CC   the presence of complex or amplification product with presence of hTRT in
CC   the sample; and (D) increasing the proliferation of a vertebrate cell by
CC   increasing hTRT expression; and (E) the use of an agent that causes an
CC   increase in cell vertebrate cell proliferation to create a medicament
CC   that inhibits ageing. A protein preparation of hTRT and the
CC   polynucleotide encoding hTRT can be used in the manufacture of
CC   medicaments for inhibiting the effect of ageing or cancer. Inhibitors of
CC   telomerase activity can be used to treat conditions that are associated
CC   with high telomerase activity. A protein preparation of hTRT can also be
CC   used in the new methods
XX
SQ   Sequence 1189 AA;

  Query Match            100.0%;  Score 5961;  DB 2;  Length 1189;
  Best Local Similarity  100.0%;  Pred. No. 0;
  Matches 1132;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 MPRAPRCRAVRSLLRSHYREVLPLATFVRRLGPQGWRLVQRGDPAAFRALVAQCLVCVPW 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         58 MPRAPRCRAVRSLLRSHYREVLPLATFVRRLGPQGWRLVQRGDPAAFRALVAQCLVCVPW 117

Qy         61 DARPPPAAPSFRQVSCLKELVARVLQRLCERGAKNVLAFGFALLDGARGGPPEAFTTSVR 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        118 DARPPPAAPSFRQVSCLKELVARVLQRLCERGAKNVLAFGFALLDGARGGPPEAFTTSVR 177

Qy        121 SYLPNTVTDALRGSGAWGLLLRRVGDDVLVHLLARCALFVLVAPSCAYQVCGPPLYQLGA 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        178 SYLPNTVTDALRGSGAWGLLLRRVGDDVLVHLLARCALFVLVAPSCAYQVCGPPLYQLGA 237

Qy        181 ATQARPPPHASGPRRRLGCERAWNHSVREAGVPLGLPAPGARRRGGSASRSLPLPKRPRR 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        238 ATQARPPPHASGPRRRLGCERAWNHSVREAGVPLGLPAPGARRRGGSASRSLPLPKRPRR 297

Qy        241 GAAPEPERTPVGQGSWAHPGRTRGPSDRGFCVVSPARPAEEATSLEGALSGTRHSHPSVG 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        298 GAAPEPERTPVGQGSWAHPGRTRGPSDRGFCVVSPARPAEEATSLEGALSGTRHSHPSVG 357

Qy        301 RQHHAGPPSTSRPPRPWDTPCPPVYAETKHFLYSSGDKEQLRPSFLLSSLRPSLTGARRL 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        358 RQHHAGPPSTSRPPRPWDTPCPPVYAETKHFLYSSGDKEQLRPSFLLSSLRPSLTGARRL 417

Qy        361 VETIFLGSRPWMPGTPRRLPRLPQRYWQMRPLFLELLGNHAQCPYGVLLKTHCPLRAAVT 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        418 VETIFLGSRPWMPGTPRRLPRLPQRYWQMRPLFLELLGNHAQCPYGVLLKTHCPLRAAVT 477

Qy        421 PAAGVCAREKPQGSVAAPEEEDTDPRRLVQLLRQHSSPWQVYGFVRACLRRLVPPGLWGS 480
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        478 PAAGVCAREKPQGSVAAPEEEDTDPRRLVQLLRQHSSPWQVYGFVRACLRRLVPPGLWGS 537

Qy        481 RHNERRFLRNTKKFISLGKHAKLSLQELTWKMSVRDCAWLRRSPGVGCVPAAEHRLREEI 540
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        538 RHNERRFLRNTKKFISLGKHAKLSLQELTWKMSVRDCAWLRRSPGVGCVPAAEHRLREEI 597

Qy        541 LAKFLHWLMSVYVVELLRSFFYVTETTFQKNRLFFYRKSVWSKLQSIGIRQHLKRVQLRE 600
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        598 LAKFLHWLMSVYVVELLRSFFYVTETTFQKNRLFFYRKSVWSKLQSIGIRQHLKRVQLRE 657

Qy        601 LSEAEVRQHREARPALLTSRLRFIPKPDGLRPIVNMDYVVGARTFRREKRAERLTSRVKA 660
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        658 LSEAEVRQHREARPALLTSRLRFIPKPDGLRPIVNMDYVVGARTFRREKRAERLTSRVKA 717

Qy        661 LFSVLNYERARRPGLLGASVLGLDDIHRAWRTFVLRVRAQDPPPELYFVKVDVTGAYDTI 720
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        718 LFSVLNYERARRPGLLGASVLGLDDIHRAWRTFVLRVRAQDPPPELYFVKVDVTGAYDTI 777

Qy        721 PQDRLTEVIASIIKPQNTYCVRRYAVVQKAAHGHVRKAFKSHVSTLTDLQPYMRQFVAHL 780
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        778 PQDRLTEVIASIIKPQNTYCVRRYAVVQKAAHGHVRKAFKSHVSTLTDLQPYMRQFVAHL 837

Qy        781 QETSPLRDAVVIEQSSSLNEASSGLFDVFLRFMCHHAVRIRGKSYVQCQGIPQGSILSTL 840
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        838 QETSPLRDAVVIEQSSSLNEASSGLFDVFLRFMCHHAVRIRGKSYVQCQGIPQGSILSTL 897

Qy        841 LCSLCYGDMENKLFAGIRRDGLLLRLVDDFLLVTPHLTHAKTFLRTLVRGVPEYGCVVNL 900
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        898 LCSLCYGDMENKLFAGIRRDGLLLRLVDDFLLVTPHLTHAKTFLRTLVRGVPEYGCVVNL 957

Qy        901 RKTVVNFPVEDEALGGTAFVQMPAHGLFPWCGLLLDTRTLEVQSDYSSYARTSIRASLTF 960
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        958 RKTVVNFPVEDEALGGTAFVQMPAHGLFPWCGLLLDTRTLEVQSDYSSYARTSIRASLTF 1017

Qy        961 NRGFKAGRNMRRKLFGVLRLKCHSLFLDLQVNSLQTVCTNIYKILLLQAYRFHACVLQLP 1020
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1018 NRGFKAGRNMRRKLFGVLRLKCHSLFLDLQVNSLQTVCTNIYKILLLQAYRFHACVLQLP 1077

Qy       1021 FHQQVWKNPTFFLRVISDTASLCYSILKAKNAGMSLGAKGAAGPLPSEAVQWLCHQAFLL 1080
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1078 FHQQVWKNPTFFLRVISDTASLCYSILKAKNAGMSLGAKGAAGPLPSEAVQWLCHQAFLL 1137

Qy       1081 KLTRHRVTYVPLLGSLRTAQTQLSRKLPGTTLTALEAAANPALPSDFKTILD 1132
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                    ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1138 KLTRHRVTYVPLLGSLRTAQTQLSRKLPGTTLTALEAAANPALPSDFKTILD 1189


RESULT 24
AAW47000
ID   AAW47000 standard; protein; 1285 AA.
XX
AC   AAW47000;
XX
DT   13-AUG-1998  (first entry)
XX
DE   HIS tagged thioredoxin moiety and full length hTRT fusion protein.
XX
KW   Human; telomerase reverse transcriptase; hTRT; TRT; diagnosis; prognosis;
KW   cell proliferation; cancer; ageing; ribonucleoprotein.
XX
OS   Synthetic.
OS   Homo sapiens.
XX
FH   Key             Location/Qualifiers
FT   Misc-difference 119. .120
FT                   /note= "enterokinase cleavage site"
FT   Region          120. .1285
FT                   /label= hTRT
FT                   /note= "full length human telomerase reverse
FT                   transcriptase"
XX
PN   GB2317891-A.
XX
PD   08-APR-1998.
XX
PF   01-OCT-1997;   97GB-00020890.
XX
PR   01-OCT-1996;   96US-00724643.
PR   18-APR-1997;   97US-00844419.
PR   25-APR-1997;   97US-00846017.
PR   06-MAY-1997;   97US-00851843.
PR   09-MAY-1997;   97US-00854050.
PR   14-AUG-1997;   97US-00911312.
PR   14-AUG-1997;   97US-00912951.
PR   14-AUG-1997;   97US-00915503.
XX
PA   (GERO-) GERON CORP.
PA   (UYTE-) UNIV TECHNOLOGY CORP.
XX
PI   Cech TR,  Lingner J,  Nakamura T,  Chapman KB,  Morin GB,  Harley CB;
PI   Andrews WH;
XX
DR   WPI; 1998-171633/16.
XX
PT   Pure and recombinant human Telomerase Reverse Transcriptase and its
PT   variants - are useful in the diagnosis, prognosis and treatment of cell
PT   proliferation conditions especially cancer and ageing.
XX
PS   Example 6; Page 223; 387pp; English.
XX
CC   The present sequence represents a fusion protein from an example of the
CC   present invention which describes human telomerase reverse transcriptase
CC   (hTRT). The present invention also describes the following methods: (A)
CC   determining whether a test compound is a modulator of hTRT, by detecting
CC   the change in hTRT recombinant protein or polynucleotide, on
CC   administration of the compound; (B) preparation of recombinant telomerase
CC   by contacting a protein preparation of hTRT with a telomerase RNA
CC   component; (C) detection of the hTRT RNA or protein in a sample by
CC   binding a relevant probe to the sample and detecting the complex formed
CC   or in the case of RNA detection, amplifying the product and correlating
CC   the presence of complex or amplification product with presence of hTRT in
CC   the sample; and (D) increasing the proliferation of a vertebrate cell by
CC   increasing hTRT expression; and (E) the use of an agent that causes an
CC   increase in cell vertebrate cell proliferation to create a medicament
CC   that inhibits ageing. A protein preparation of hTRT and the
CC   polynucleotide encoding hTRT can be used in the manufacture of
CC   medicaments for inhibiting the effect of ageing or cancer. Inhibitors of
CC   telomerase activity can be used to treat conditions that are associated
CC   with high telomerase activity. A protein preparation of hTRT can also be
CC   used in the new methods
XX
SQ   Sequence 1285 AA;

  Query Match             99.9%;  Score 5955;  DB 2;  Length 1285;
  Best Local Similarity   99.9%;  Pred. No. 0;
  Matches 1131;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          1 MPRAPRCRAVRSLLRSHYREVLPLATFVRRLGPQGWRLVQRGDPAAFRALVAQCLVCVPW 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        154 MPRAPRCRAVRSLLRSHYREVLPLATFVRRLGPQGWRLVQRGDPAAFRALVAQCLVCVPW 213

Qy         61 DARPPPAAPSFRQVSCLKELVARVLQRLCERGAKNVLAFGFALLDGARGGPPEAFTTSVR 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        214 DARPPPAAPSFRQVSCLKELVARVLQRLCERGAKNVLAFGFALLDGARGGPPEAFTTSVR 273

Qy        121 SYLPNTVTDALRGSGAWGLLLRRVGDDVLVHLLARCALFVLVAPSCAYQVCGPPLYQLGA 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        274 SYLPNTVTDALRGSGAWGLLLRRVGDDVLVHLLARCALFVLVAPSCAYQVCGPPLYQLGA 333

Qy        181 ATQARPPPHASGPRRRLGCERAWNHSVREAGVPLGLPAPGARRRGGSASRSLPLPKRPRR 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        334 ATQARPPPHASGPRRRLGCERAWNHSVREAGVPLGLPAPGARRRGGSASRSLPLPKRPRR 393

Qy        241 GAAPEPERTPVGQGSWAHPGRTRGPSDRGFCVVSPARPAEEATSLEGALSGTRHSHPSVG 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        394 GAAPEPERTPVGQGSWAHPGRTRGPSDRGFCVVSPARPAEEATSLEGALSGTRHSHPSVG 453

Qy        301 RQHHAGPPSTSRPPRPWDTPCPPVYAETKHFLYSSGDKEQLRPSFLLSSLRPSLTGARRL 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        454 RQHHAGPPSTSRPPRPWDTPCPPVYAETKHFLYSSGDKEQLRPSFLLSSLRPSLTGARRL 513

Qy        361 VETIFLGSRPWMPGTPRRLPRLPQRYWQMRPLFLELLGNHAQCPYGVLLKTHCPLRAAVT 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        514 VETIFLGSRPWMPGTPRRLPRLPQRYWQMRPLFLELLGNHAQCPYGVLLKTHCPLRAAVT 573

Qy        421 PAAGVCAREKPQGSVAAPEEEDTDPRRLVQLLRQHSSPWQVYGFVRACLRRLVPPGLWGS 480
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        574 PAAGVCAREKPQGSVAAPEEEDTDPRRLVQLLRQHSSPWQVYGFVRACLRRLVPPGLWGS 633

Qy        481 RHNERRFLRNTKKFISLGKHAKLSLQELTWKMSVRDCAWLRRSPGVGCVPAAEHRLREEI 540
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        634 RHNERRFLRNTKKFISLGKHAKLSLQELTWKMSVRDCAWLRRSPGVGCVPAAEHRLREEI 693

Qy        541 LAKFLHWLMSVYVVELLRSFFYVTETTFQKNRLFFYRKSVWSKLQSIGIRQHLKRVQLRE 600
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        694 LAKFLHWLMSVYVVELLRSFFYVTETTFQKNRLFFYRKSVWSKLQSIGIRQHLKRVQLRE 753

Qy        601 LSEAEVRQHREARPALLTSRLRFIPKPDGLRPIVNMDYVVGARTFRREKRAERLTSRVKA 660
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        754 LSEAEVRQHREARPALLTSRLRFIPKPDGLRPIVNMDYVVGARTFRREKRAERLTSRVKA 813

Qy        661 LFSVLNYERARRPGLLGASVLGLDDIHRAWRTFVLRVRAQDPPPELYFVKVDVTGAYDTI 720
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        814 LFSVLNYERARRPGLLGASVLGLDDIHRAWRTFVLRVRAQDPPPELYFVKVDVTGAYDTI 873

Qy        721 PQDRLTEVIASIIKPQNTYCVRRYAVVQKAAHGHVRKAFKSHVSTLTDLQPYMRQFVAHL 780
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        874 PQDRLTEVIASIIKPQNTYCVRRYAVVQKAAHGHVRKAFKSHVSTLTDLQPYMRQFVAHL 933

Qy        781 QETSPLRDAVVIEQSSSLNEASSGLFDVFLRFMCHHAVRIRGKSYVQCQGIPQGSILSTL 840
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        934 QETSPLRDAVVIEQSSSLNEASSGLFDVFLRFMCHHAVRIRGKSYVQCQGIPQGSILSTL 993

Qy        841 LCSLCYGDMENKLFAGIRRDGLLLRLVDDFLLVTPHLTHAKTFLRTLVRGVPEYGCVVNL 900
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        994 LCSLCYGDMENKLFAGIRRDGLLLRLVDDFLLVTPHLTHAKTFLRTLVRGVPEYGCVVNL 1053

Qy        901 RKTVVNFPVEDEALGGTAFVQMPAHGLFPWCGLLLDTRTLEVQSDYSSYARTSIRASLTF 960
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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```
Db       1054 RKTVVNFPVEDEALGGTAFVQMPAHGLFPWCGLLLDTRTLEVQSDYSSYARTSIRASLTF 1113

Qy        961 NRGFKAGRNMRRKLFGVLRLKCHSLFLDLQVNSLQTVCTNIYKILLLQAYRFHACVLQLP 1020
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1114 NRGFKAGRNMRRKLFGVLRLKCHSLFLDLQVNSLQTVCTNIYKILLLQAYRFHACVLQLP 1173

Qy       1021 FHQQVWKNPTFFLRVISDTASLCYSILKAKNAGMSLGAKGAAGPLPSEAVQWLCHQAFLL 1080
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1174 FHQQVWKNPTFFLRVISDTASLCYSILKAKNAGMSLGAKGAAGPLPSEAVQWLCHQAFLL 1233

Qy       1081 KLTRHRVTYVPLLGSLRTAQTQLSRKLPGTTLTALEAAANPALPSDFKTILD 1132
              |||||||||||| |||||||||||||||||||||||||||||||||||||
Db       1234 KLTRHRVTYVPLLSSLRTAQTQLSRKLPGTTLTALEAAANPALPSDFKTILD 1285
```

RESULT 25
AAW71376
ID AAW71376 standard; protein; 1132 AA.
XX
AC AAW71376;
XX
DT 04-DEC-1998 (first entry)
XX
DE Human telomerase catalytic subunit referred to as hEST2.
XX
KW Catalytic subunit; human; telomerase; telomere maintenance; diagnosis;
KW treatment; cancer.
XX
OS Homo sapiens.
XX
PN WO9837181-A2.
XX
PD 27-AUG-1998.
XX
PF 20-FEB-1998; 98WO-US003404.
XX
PR 20-FEB-1997; 97US-0038750P.
PR 20-MAY-1997; 97US-0047151P.
PR 01-AUG-1997; 97US-0054549P.
PR 14-AUG-1997; 97US-0055762P.
PR 30-OCT-1997; 97US-0064322P.
XX
PA (WHED) WHITEHEAD INST BIOMEDICAL RES.
XX
PI Counter CM, Meyerson M, Weinberg RA;
XX
DR WPI; 1998-495367/42.
DR N-PSDB; AAV60320.
XX
PT New isolated human telomerase catalytic sub-unit gene - used to develop
PT products for increasing or reducing the life span of cells such as cancer
PT cells or transformed cells.
XX
PS Claim 5; Fig 6; 96pp; English.
XX
CC The present sequence represents the catalytic subunit of a human
CC telomerase holoenzyme. Disruption of the telomerase gene alters telomere
CC maintenance. The DNA is essential for telomerase activity, and the
CC protein is physically associated with telomerase and a constituent of
CC active telomerase complex. The products can be used for increasing or
CC reducing the lifespan of cells such as cancer cells or transformed cells.
CC They can also be used in the diagnosis and treatment of malignancies. In
CC addition, cells with a longer lifespan can be transplanted into or
CC grafted onto an individual (e.g. as skin grafts, as systems for delivery
CC of therapeutic proteins, such as hormones and enzymes), to whom they
CC provide therapeutic benefit
XX
SQ Sequence 1132 AA;

Query Match 99.9%; Score 5954; DB 2; Length 1132;
Best Local Similarity 99.9%; Pred. No. 0;
Matches 1131; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

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Qy          1 MPRAPRCRAVRSLLRSHYREVLPLATFVRRLGPQGWRLVQRGDPAAFRALVAQCLVCVPW 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 MPRAPRCRAVRSLLRSHYREVLPLATFVRRLGPQGWRLVQRGDPAAFRALVAQCLVCVPW 60

Qy         61 DARPPPAAPSFRQVSCLKELVARVLQRLCERGAKNVLAFGFALLDGARGGPPEAFTTSVR 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 DARPPPAAPSFRQVSCLKELVARVLQRLCERGAKNVLAFGFALLDGARGGPPEAFTTSVR 120

Qy        121 SYLPNTVTDALRGSGAWGLLLRRVGDDVLVHLLARCALFVLVAPSCAYQVCGPPLYQLGA 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 SYLPNTVTDALRGSGAWGLLLRRVGDDVLVHLLARCALFVLVAPSCAYQVCGPPLYQLGA 180

Qy        181 ATQARPPPHASGPRRRLGCERAWNHSVREAGVPLGLPAPGARRRGGSASRSLPLPKRPRR 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 ATQARPPPHASGPRRRLGCERAWNHSVREAGVPLGLPAPGARRRGGSASRSLPLPKRPRR 240

Qy        241 GAAPEPERTPVGQGSWAHPGRTRGPSDRGFCVVSPARPAEEATSLEGALSGTRHSHPSVG 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 GAAPEPERTPVGQGSWAHPGRTRGPSDRGFCVVSPARPAEEATSLEGALSGTRHSHPSVG 300

Qy        301 RQHHAGPPSTSRPPRPWDTPCPPVYAETKHFLYSSGDKEQLRPSFLLSSLRPSLTGARRL 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 RQHHAGPPSTSRPPRPWDTPCPPVYAETKHFLYSSGDKEQLRPSFLLSSLRPSLTGARRL 360

Qy        361 VETIFLGSRPWMPGTPRRLPRLPQRYWQMRPLFLELLGNHAQCPYGVLLKTHCPLRAAVT 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        361 VETIFLGSRPWMPGTPRRLPRLPQRYWQMRPLFLELLGNHAQCPYGVLLKTHCPLRAAVT 420

Qy        421 PAAGVCAREKPQGSVAAPEEEDTDPRRLVQLLRQHSSPWQVYGFVRACLRRLVPPGLWGS 480
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        421 PAAGVCAREKPQGSVAAPEEEDTDPRRLVQLLRQHSSPWQVYGFVRACLRRLVPPGLWGS 480

Qy        481 RHNERRFLRNTKKFISLGKHAKLSLQELTWKMSVRDCAWLRRSPGVGCVPAAEHRLREEI 540
              |||||||||||||||||||||||||||||| ||||||||||||||||||||||||||||
Db        481 RHNERRFLRNTKKFISLGKHAKLSLQELTWKMSVRGCAWLRRSPGVGCVPAAEHRLREEI 540

Qy        541 LAKFLHWLMSVYVVELLRSFFYVTETTFQKNRLFFYRKSVWSKLQSIGIRQHLKRVQLRE 600
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        541 LAKFLHWLMSVYVVELLRSFFYVTETTFQKNRLFFYRKSVWSKLQSIGIRQHLKRVQLRE 600

Qy        601 LSEAEVRQHREARPALLTSRLRFIPKPDGLRPIVNMDYVVGARTFRREKRAERLTSRVKA 660
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        601 LSEAEVRQHREARPALLTSRLRFIPKPDGLRPIVNMDYVVGARTFRREKRAERLTSRVKA 660

Qy        661 LFSVLNYERARRPGLLGASVLGLDDIHRAWRTFVLRVRAQDPPPELYFVKVDVTGAYDTI 720
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        661 LFSVLNYERARRPGLLGASVLGLDDIHRAWRTFVLRVRAQDPPPELYFVKVDVTGAYDTI 720

Qy        721 PQDRLTEVIASIIKPQNTYCVRRYAVVQKAAHGHVRKAFKSHVSTLTDLQPYMRQFVAHL 780
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        721 PQDRLTEVIASIIKPQNTYCVRRYAVVQKAAHGHVRKAFKSHVSTLTDLQPYMRQFVAHL 780

Qy        781 QETSPLRDAVVIEQSSSLNEASSGLFDVFLRFMCHHAVRIRGKSYVQCQGIPQGSILSTL 840
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        781 QETSPLRDAVVIEQSSSLNEASSGLFDVFLRFMCHHAVRIRGKSYVQCQGIPQGSILSTL 840

Qy        841 LCSLCYGDMENKLFAGIRRDGLLLRLVDDFLLVTPHLTHAKTFLRTLVRGVPEYGCVVNL 900
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        841 LCSLCYGDMENKLFAGIRRDGLLLRLVDDFLLVTPHLTHAKTFLRTLVRGVPEYGCVVNL 900

Qy        901 RKTVVNFPVEDEALGGTAFVQMPAHGLFPWCGLLLDTRTLEVQSDYSSYARTSIRASLTF 960
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        901 RKTVVNFPVEDEALGGTAFVQMPAHGLFPWCGLLLDTRTLEVQSDYSSYARTSIRASLTF 960

Qy        961 NRGFKAGRNMRRKLFGVLRLKCHSLFLDLQVNSLQTVCTNIYKILLLQAYRFHACVLQLP 1020
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        961 NRGFKAGRNMRRKLFGVLRLKCHSLFLDLQVNSLQTVCTNIYKILLLQAYRFHACVLQLP 1020

Qy       1021 FHQQVWKNPTFFLRVISDTASLCYSILKAKNAGMSLGAKGAAGPLPSEAVQWLCHQAFLL 1080
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1021 FHQQVWKNPTFFLRVISDTASLCYSILKAKNAGMSLGAKGAAGPLPSEAVQWLCHQAFLL 1080

Qy       1081 KLTRHRVTYVPLLGSLRTAQTQLSRKLPGTTLTALEAAANPALPSDFKTILD 1132
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                 ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1081 KLTRHRVTYVPLLGSLRTAQTQLSRKLPGTTLTALEAAANPALPSDFKTILD 1132

RESULT 26
AAY00627
ID   AAY00627 standard; protein; 1132 AA.
XX
AC   AAY00627;
XX
DT   26-JUL-1999  (first entry)
XX
DE   Human telomerase protein sequence.
XX
KW   Telomerase; human; cancer; diagnosis; melanoma; skin cancer; leukaemia;
KW   neuroblastoma; breast carcinoma; colon carcinoma; lymphoma; osteosarcoma;
KW   smooth muscle cell hyperplasia; stem cell proliferation; Wilm's tumour;
KW   stem cell differentiation; organ regeneration; organ differentiation.
XX
OS   Homo sapiens.
XX
PN   WO9901560-A1.
XX
PD   14-JAN-1999.
XX
PF   01-JUL-1998;   98WO-US013835.
XX
PR   01-JUL-1997;   97US-0051410P.
PR   21-JUL-1997;   97US-0053018P.
PR   21-JUL-1997;   97US-0053329P.
PR   04-AUG-1997;   97US-0054642P.
PR   09-SEP-1997;   97US-0058287P.
XX
PA   (CAMB-) CAMBIA BIOSYSTEMS LLC.
XX
PI   Kilian A,  Bowtell D;
XX
DR   WPI; 1999-106060/09.
DR   N-PSDB; AAX18254.
XX
PT   New isolated vertebrate telomerase genes - used to develop products for
PT   treating cancers or for organ regeneration, nerve cell or brain cell
PT   growth following injury or bone marrow transplantation.
XX
PS   Claim 19; Fig 1; 134pp; English.
XX
CC   This sequence is the human telomerase of the invention. Primers that
CC   amplify the telomerase coding sequence can be used in a method for
CC   diagnosing cancer in a patient. The telomerase can be used for detection,
CC   diagnosis and drug screening. Inhibitors of telomerase activity can be
CC   used to treat cancers such as melanomas, other skin cancers,
CC   neuroblastomas, breast carcinomas, colon carcinomas, leukaemias,
CC   lymphomas, osteosarcomas or smooth muscle cell hyperplasias or skin
CC   growths. Enhancers of telomerase may be used to stimulate stem cell
CC   proliferation and differentiation (expansion of haematopoietic stem cells
CC   could be administered in the bone marrow transplant context). As well,
CC   many tissues have stem cells. Proliferation of these cells may be useful
CC   in wound healing, hair growth, treatment of disease such as Wilm's
CC   tumour, organ regeneration or differentiation after injury or diseases,
CC   nerve cell or brain cell growth following injury
XX
SQ   Sequence 1132 AA;

  Query Match             99.9%;  Score 5954;  DB 2;  Length 1132;
  Best Local Similarity   99.9%;  Pred. No. 0;
  Matches 1131;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          1 MPRAPRCRAVRSLLRSHYREVLPLATFVRRLGPQGWRLVQRGDPAAFRALVAQCLVCVPW 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 MPRAPRCRAVRSLLRSHYREVLPLATFVRRLGPQGWRLVQRGDPAAFRALVAQCLVCVPW 60

Qy         61 DARPPPAAPSFRQVSCLKELVARVLQRLCERGAKNVLAFGFALLDGARGGPPEAFTTSVR 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 DARPPPAAPSFRQVSCLKELVARVLQRLCERGAKNVLAFGFALLDGARGGPPEAFTTSVR 120

Qy        121 SYLPNTVTDALRGSGAWGLLLRRVGDDVLVHLLARCALFVLVAPSCAYQVCGPPLYQLGA 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 SYLPNTVTDALRGSGAWGLLLRRVGDDVLVHLLARCALFVLVAPSCAYQVCGPPLYQLGA 180

Qy        181 ATQARPPPHASGPRRRLGCERAWNHSVREAGVPLGLPAPGARRRGGSASRSLPLPKRPRR 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 ATQARPPPHASGPRRRLGCERAWNHSVREAGVPLGLPAPGARRRGGSASRSLPLPKRPRR 240

Qy        241 GAAPEPERTPVGQGSWAHPGRTRGPSDRGFCVVSPARPAEEATSLEGALSGTRHSHPSVG 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 GAAPEPERTPVGQGSWAHPGRTRGPSDRGFCVVSPARPAEEATSLEGALSGTRHSHPSVG 300

Qy        301 RQHHAGPPSTSRPPRPWDTPCPPVYAETKHFLYSSGDKEQLRPSFLLSSLRPSLTGARRL 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 RQHHAGPPSTSRPPRPWDTPCPPVYAETKHFLYSSGDKEQLRPSFLLSSLRPSLTGARRL 360

Qy        361 VETIFLGSRPWMPGTPRRLPRLPQRYWQMRPLFLELLGNHAQCPYGVLLKTHCPLRAAVT 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        361 VETIFLGSRPWMPGTPRRLPRLPQRYWQMRPLFLELLGNHAQCPYGVLLKTHCPLRAAVT 420

Qy        421 PAAGVCAREKPQGSVAAPEEEDTDPRRLVQLLRQHSSPWQVYGFVRACLRRLVPPGLWGS 480
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        421 PAAGVCAREKPQGSVAAPEEEDTDPRRLVQLLRQHSSPWQVYGFVRACLRRLVPPGLWGS 480

Qy        481 RHNERRFLRNTKKFISLGKHAKLSLQELTWKMSVRDCAWLRRSPGVGCVPAAEHRLREEI 540
              ||||||||||||||||||||||||||||||||||| ||||||||||||||||||||||||
Db        481 RHNERRFLRNTKKFISLGKHAKLSLQELTWKMSVRGCAWLRRSPGVGCVPAAEHRLREEI 540

Qy        541 LAKFLHWLMSVYVVELLRSFFYVTETTFQKNRLFFYRKSVWSKLQSIGIRQHLKRVQLRE 600
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        541 LAKFLHWLMSVYVVELLRSFFYVTETTFQKNRLFFYRKSVWSKLQSIGIRQHLKRVQLRE 600

Qy        601 LSEAEVRQHREARPALLTSRLRFIPKPDGLRPIVNMDYVVGARTFRREKRAERLTSRVKA 660
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        601 LSEAEVRQHREARPALLTSRLRFIPKPDGLRPIVNMDYVVGARTFRREKRAERLTSRVKA 660

Qy        661 LFSVLNYERARRPGLLGASVLGLDDIHRAWRTFVLRVRAQDPPPELYFVKVDVTGAYDTI 720
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        661 LFSVLNYERARRPGLLGASVLGLDDIHRAWRTFVLRVRAQDPPPELYFVKVDVTGAYDTI 720

Qy        721 PQDRLTEVIASIIKPQNTYCVRRYAVVQKAAHGHVRKAFKSHVSTLTDLQPYMRQFVAHL 780
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        721 PQDRLTEVIASIIKPQNTYCVRRYAVVQKAAHGHVRKAFKSHVSTLTDLQPYMRQFVAHL 780

Qy        781 QETSPLRDAVVIEQSSSLNEASSGLFDVFLRFMCHHAVRIRGKSYVQCQGIPQGSILSTL 840
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        781 QETSPLRDAVVIEQSSSLNEASSGLFDVFLRFMCHHAVRIRGKSYVQCQGIPQGSILSTL 840

Qy        841 LCSLCYGDMENKLFAGIRRDGLLLRLVDDFLLVTPHLTHAKTFLRTLVRGVPEYGCVVNL 900
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        841 LCSLCYGDMENKLFAGIRRDGLLLRLVDDFLLVTPHLTHAKTFLRTLVRGVPEYGCVVNL 900

Qy        901 RKTVVNFPVEDEALGGTAFVQMPAHGLFPWCGLLLDTRTLEVQSDYSSYARTSIRASLTF 960
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        901 RKTVVNFPVEDEALGGTAFVQMPAHGLFPWCGLLLDTRTLEVQSDYSSYARTSIRASLTF 960

Qy        961 NRGFKAGRNMRRKLFGVLRLKCHSLFLDLQVNSLQTVCTNIYKILLLQAYRFHACVLQLP 1020
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        961 NRGFKAGRNMRRKLFGVLRLKCHSLFLDLQVNSLQTVCTNIYKILLLQAYRFHACVLQLP 1020

Qy       1021 FHQQVWKNPTFFLRVISDTASLCYSILKAKNAGMSLGAKGAAGPLPSEAVQWLCHQAFLL 1080
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1021 FHQQVWKNPTFFLRVISDTASLCYSILKAKNAGMSLGAKGAAGPLPSEAVQWLCHQAFLL 1080

Qy       1081 KLTRHRVTYVPLLGSLRTAQTQLSRKLPGTTLTALEAAANPALPSDFKTILD 1132
              ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1081 KLTRHRVTYVPLLGSLRTAQTQLSRKLPGTTLTALEAAANPALPSDFKTILD 1132

RESULT 27
AAY00638
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```
ID   AAY00638 standard; protein; 1132 AA.
XX
AC   AAY00638;
XX
DT   26-JUL-1999  (first entry)
XX
DE   Truncated telomerase protein sequence.
XX
KW   Telomerase; human; cancer; diagnosis; melanoma; skin cancer; leukaemia;
KW   neuroblastoma; breast carcinoma; colon carcinoma; lymphoma; osteosarcoma;
KW   smooth muscle cell hyperplasia; stem cell proliferation; Wilm's tumour;
KW   stem cell differentiation; organ regeneration; organ differentiation.
XX
OS   Homo sapiens.
OS   Synthetic.
XX
PN   WO9901560-A1.
XX
PD   14-JAN-1999.
XX
PF   01-JUL-1998;   98WO-US013835.
XX
PR   01-JUL-1997;   97US-0051410P.
PR   21-JUL-1997;   97US-0053018P.
PR   21-JUL-1997;   97US-0053329P.
PR   04-AUG-1997;   97US-0054642P.
PR   09-SEP-1997;   97US-0058287P.
XX
PA   (CAMB-) CAMBIA BIOSYSTEMS LLC.
XX
PI   Kilian A,  Bowtell D;
XX
DR   WPI; 1999-106060/09.
DR   N-PSDB; AAX18266.
XX
PT   New isolated vertebrate telomerase genes - used to develop products for
PT   treating cancers or for organ regeneration, nerve cell or brain cell
PT   growth following injury or bone marrow transplantation.
XX
PS   Claim 4; Fig 11f-i; 134pp; English.
XX
CC   This sequence is a truncated human telomerase of the invention. Primers
CC   that amplify the telomerase coding sequence can be used in a method for
CC   diagnosing cancer in a patient. The telomerase can be used for detection,
CC   diagnosis and drug screening. Inhibitors of telomerase activity can be
CC   used to treat cancers such as melanomas, other skin cancers,
CC   neuroblastomas, breast carcinomas, colon carcinomas, leukaemias,
CC   lymphomas, osteosarcomas or smooth muscle cell hyperplasias or skin
CC   growths. Enhancers of telomerase may be used to stimulate stem cell
CC   proliferation and differentiation (expansion of haematopoietic stem cells
CC   could be administered in the bone marrow transplant context). As well,
CC   many tissues have stem cells. Proliferation of these cells may be useful
CC   in wound healing, hair growth, treatment of disease such as Wilm's
CC   tumour, organ regeneration or differentiation after injury or diseases,
CC   nerve cell or brain cell growth following injury
XX
SQ   Sequence 1132 AA;

  Query Match             99.9%;  Score 5954;  DB 2;  Length 1132;
  Best Local Similarity   99.9%;  Pred. No. 0;
  Matches 1131;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          1 MPRAPRCRAVRSLLRSHYREVLPLATFVRRLGPQGWRLVQRGDPAAFRALVAQCLVCVPW 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 MPRAPRCRAVRSLLRSHYREVLPLATFVRRLGPQGWRLVQRGDPAAFRALVAQCLVCVPW 60

Qy         61 DARPPPAAPSFRQVSCLKELVARVLQRLCERGAKNVLAFGFALLDGARGGPPEAFTTSVR 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 DARPPPAAPSFRQVSCLKELVARVLQRLCERGAKNVLAFGFALLDGARGGPPEAFTTSVR 120

Qy        121 SYLPNTVTDALRGSGAWGLLLRRVGDDVLVHLLARCALFVLVAPSCAYQVCGPPLYQLGA 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 SYLPNTVTDALRGSGAWGLLLRRVGDDVLVHLLARCALFVLVAPSCAYQVCGPPLYQLGA 180

Qy        181 ATQARPPPHASGPRRRLGCERAWNHSVREAGVPLGLPAPGARRRGGSASRSLPLPKRPRR 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 ATQARPPPHASGPRRRLGCERAWNHSVREAGVPLGLPAPGARRRGGSASRSLPLPKRPRR 240

Qy        241 GAAPEPERTPVGQGSWAHPGRTRGPSDRGFCVVSPARPAEEATSLEGALSGTRHSHPSVG 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 GAAPEPERTPVGQGSWAHPGRTRGPSDRGFCVVSPARPAEEATSLEGALSGTRHSHPSVG 300

Qy        301 RQHHAGPPSTSRPPRPWDTPCPPVYAETKHFLYSSGDKEQLRPSFLLSSLRPSLTGARRL 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 RQHHAGPPSTSRPPRPWDTPCPPVYAETKHFLYSSGDKEQLRPSFLLSSLRPSLTGARRL 360

Qy        361 VETIFLGSRPWMPGTPRRLPRLPQRYWQMRPLFLELLGNHAQCPYGVLLKTHCPLRAAVT 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        361 VETIFLGSRPWMPGTPRRLPRLPQRYWQMRPLFLELLGNHAQCPYGVLLKTHCPLRAAVT 420

Qy        421 PAAGVCAREKPQGSVAAPEEEDTDPRRLVQLLRQHSSPWQVYGFVRACLRRLVPPGLWGS 480
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        421 PAAGVCAREKPQGSVAAPEEEDTDPRRLVQLLRQHSSPWQVYGFVRACLRRLVPPGLWGS 480

Qy        481 RHNERRFLRNTKKFISLGKHAKLSLQELTWKMSVRDCAWLRRSPGVGCVPAAEHRLREEI 540
              ||||||||||||||||||||||||||||||||| ||||||||||||||||||||||||||
Db        481 RHNERRFLRNTKKFISLGKHAKLSLQELTWKMSVRGCAWLRRSPGVGCVPAAEHRLREEI 540

Qy        541 LAKFLHWLMSVYVVELLRSFFYVTETTFQKNRLFFYRKSVWSKLQSIGIRQHLKRVQLRE 600
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        541 LAKFLHWLMSVYVVELLRSFFYVTETTFQKNRLFFYRKSVWSKLQSIGIRQHLKRVQLRE 600

Qy        601 LSEAEVRQHREARPALLTSRLRFIPKPDGLRPIVNMDYVVGARTFRREKRAERLTSRVKA 660
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        601 LSEAEVRQHREARPALLTSRLRFIPKPDGLRPIVNMDYVVGARTFRREKRAERLTSRVKA 660

Qy        661 LPSVLNYERARRPGLLGASVLGLDDIHRAWRTFVLRVRAQDPPPELYFVKVDVTGAYDTI 720
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        661 LFSVLNYERARRPGLLGASVLGLDDIHRAWRTFVLRVRAQDPPPELYFVKVDVTGAYDTI 720

Qy        721 PQDRLTEVIASIIKPQNTYCVRRYAVVQKAAHGHVRKAFKSHVSTLTDLQPYMRQFVAHL 780
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        721 PQDRLTEVIASIIKPQNTYCVRRYAVVQKAAHGHVRKAFKSHVSTLTDLQPYMRQFVAHL 780

Qy        781 QETSPLRDAVVIEQSSSLNEASSGLFDVFLRFMCHHAVRIRGKSYVQCQGIPQGSILSTL 840
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        781 QETSPLRDAVVIEQSSSLNEASSGLFDVFLRFMCHHAVRIRGKSYVQCQGIPQGSILSTL 840

Qy        841 LCSLCYGDMENKLFAGIRRDGLLLRLVDDFLLVTPHLTHAKTFLRTLVRGVPEYGCVVNL 900
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        841 LCSLCYGDMENKLFAGIRRDGLLLRLVDDFLLVTPHLTHAKTFLRTLVRGVPEYGCVVNL 900

Qy        901 RKTVVNFPVEDEALGGTAFVQMPAHGLFPWCGLLLDTRTLEVQSDYSSYARTSIRASLTF 960
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        901 RKTVVNFPVEDEALGGTAFVQMPAHGLFPWCGLLLDTRTLEVQSDYSSYARTSIRASLTF 960

Qy        961 NRGFKAGRNMRRKLFGVLRLKCHSLFLDLQVNSLQTVCTNIYKILLLQAYRFHACVLQLP 1020
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        961 NRGFKAGRNMRRKLFGVLRLKCHSLFLDLQVNSLQTVCTNIYKILLLQAYRFHACVLQLP 1020

Qy       1021 FHQQVWKNPTFFLRVISDTASLCYSILKAKNAGMSLGAKGAAGPLPSEAVQWLCHQAFLL 1080
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1021 FHQQVWKNPTFFLRVISDTASLCYSILKAKNAGMSLGAKGAAGPLPSEAVQWLCHQAFLL 1080

Qy       1081 KLTRHRVTYVPLLGSLRTAQTQLSRKLPGTTLTALEAAANPALPSDFKTILD 1132
              ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1081 KLTRHRVTYVPLLGSLRTAQTQLSRKLPGTTLTALEAAANPALPSDFKTILD 1132


RESULT 28
AAY28401
ID   AAY28401 standard; protein; 1132 AA.
XX
AC   AAY28401;
XX
DT   22-SEP-1999  (first entry)
```

XX
DE Human EST2 protein sequence.
XX
KW EST2; proliferative capacity; cellular proliferation; decubitus ulcer;
KW telomerase-activating therapeutic agent; cell life-span extension;
KW venous disease; venous stasis ulcer; excessive pressure; arterial ulcer;
KW tissue regeneration enhancer; atherosclerosis; therapy.
XX
OS Homo sapiens.
XX
PN WO9935243-A2.
XX
PD 15-JUL-1999.
XX
PF 12-JAN-1999; 99WO-US000682.
XX
PR 12-JAN-1998; 98US-0071220P.
PR 13-JAN-1998; 98US-0071455P.
PR 21-APR-1998; 98US-00063657.
XX
PA (COLD-) COLD SPRING HARBOR LAB.
XX
PI Hannon GJ, Wang J, Beach DH;
XX
DR WPI; 1999-444196/37.
DR N-PSDB; AAX89424.
XX
PT Increasing proliferative capacity of cells useful for promoting wound
PT healing.
XX
PS Claim 3; Page 65-70; 73pp; English.
XX
CC This sequence is the human EST2 protein, and can be used in the method of
CC the invention. The method is for increasing the proliferative capacity of
CC cells , and comprises contacting the cell with a telomerase-activating
CC therapeutic agent (TATA). The method can be used for extending the life-
CC span of cells, e.g. by increasing the number of mitotic divisions. They
CC can be used for e.g. the extension of skin or other epithelial cell
CC cultures or grafts, the expansion of mesenchymal cell cultures or grafts,
CC and the expansion of chondrocyte or osteocyte cultures or grafts. They
CC can be applied to e.g. neuronal, haematopoietic, epithelial, pancreatic,
CC hepatic, chondrocytic and osteocytic stem and progenitor cells in in
CC vivo, in vitro or ex vivo protocols. The methods can be used for
CC promoting the healing of wounds resulting from e.g. surgery, burns,
CC inflammation or irritation or ulcers resulting from e.g. venous disease
CC (venous stasis ulcers), excessive pressure (decubitus ulcers) or arterial
CC ulcers. They can also be used to enhance tissue regeneration processes,
CC e.g. of the skin, hair and/or fingernails. They can also be used for
CC treating age-related conditions, e.g. atrophy of the skin through loss of
CC extracellular matrix homeostasis in dermal fibroblasts, age-related
CC macular degeneration caused by accumulation of liofuscin and
CC downregulation of a neuronal survival factor in retinal pigmented
CC epithelial (RPE) cells, and atherosclerosis caused by loss of
CC proliferative capacity and overexpression of hypertensive and thrombotic
CC factors in endothelial cells. Expanded populations of normal or
CC genetically engineered rejuvenated cells could be used for autologous or
CC allogeneic cell and gene therapy. They can also be used for prolonging
CC the lifespan of a culture of normal cells or tissue being used to secrete
CC therapeutic or other commercially significant proteins and products
XX
SQ Sequence 1132 AA;

Query Match 99.9%; Score 5954; DB 2; Length 1132;
Best Local Similarity 99.9%; Pred. No. 0;
Matches 1131; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

```
Qy          1 MPRAPRCRAVRSLLRSHYREVLPLATFVRRLGPQGWRLVQRGDPAAFRALVAQCLVCVPW 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 MPRAPRCRAVRSLLRSHYREVLPLATFVRRLGPQGWRLVQRGDPAAFRALVAQCLVCVPW 60

Qy         61 DARPPPAAPSFRQVSCLKELVARVLQRLCERGAKNVLAFGFALLDGARGGPPEAFTTSVR 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 DARPPPAAPSFRQVSCLKELVARVLQRLCERGAKNVLAFGFALLDGARGGPPEAFTTSVR 120

Qy        121 SYLPNTVTDALRGSGAWGLLLRRVGDDVLVHLLARCALFVLVAPSCAYQVCGPPLYQLGA 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 SYLPNTVTDALRGSGAWGLLLRRVGDDVLVHLLARCALFVLVAPSCAYQVCGPPLYQLGA 180

Qy        181 ATQARPPPHASGPRRRLGCERAWNHSVREAGVPLGLPAPGARRRGGSASRSLPLPKRPRR 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 ATQARPPPHASGPRRRLGCERAWNHSVREAGVPLGLPAPGARRRGGSASRSLPLPKRPRR 240

Qy        241 GAAPEPERTPVGQGSWAHPGRTRGPSDRGFCVVSPARPAEEATSLEGALSGTRHSHPSVG 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 GAAPEPERTPVGQGSWAHPGRTRGPSDRGFCVVSPARPAEEATSLEGALSGTRHSHPSVG 300

Qy        301 RQHHAGPPSTSRPPRPWDTPCPPVYAETKHFLYSSGDKEQLRPSFLLSSLRPSLTGARRL 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 RQHHAGPPSTSRPPRPWDTPCPPVYAETKHFLYSSGDKEQLRPSFLLSSLRPSLTGARRL 360

Qy        361 VETIFLGSRPWMPGTPRRLPRLPQRYWQMRPLFLELLGNHAQCPYGVLLKTHCPLRAAVT 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        361 VETIFLGSRPWMPGTPRRLPRLPQRYWQMRPLFLELLGNHAQCPYGVLLKTHCPLRAAVT 420

Qy        421 PAAGVCAREKPQGSVAAPEEEDTDPRRLVQLLRQHSSPWQVYGFVRACLRRLVPPGLWGS 480
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        421 PAAGVCAREKPQGSVAAPEEEDTDPRRLVQLLRQHSSPWQVYGFVRACLRRLVPPGLWGS 480

Qy        481 RHNERRFLRNTKKFISLGKHAKLSLQELTWKMSVRDCAWLRRSPGVGCVPAAEHRLREEI 540
              ||||||||||||||||||||||||||||||||||| ||||||||||||||||||||||||
Db        481 RHNERRFLRNTKKFISLGKHAKLSLQELTWKMSVRGCAWLRRSPGVGCVPAAEHRLREEI 540

Qy        541 LAKFLHWLMSVYVVELLRSFFYVTETTFQKNRLFFYRKSVWSKLQSIGIRQHLKRVQLRE 600
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        541 LAKFLHWLMSVYVVELLRSFFYVTETTFQKNRLFFYRKSVWSKLQSIGIRQHLKRVQLRE 600

Qy        601 LSEAEVRQHREARPALLTSRLRFIPKPDGLRPIVNMDYVVGARTFRREKRAERLTSRVKA 660
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        601 LSEAEVRQHREARPALLTSRLRFIPKPDGLRPIVNMDYVVGARTFRREKRAERLTSRVKA 660

Qy        661 LFSVLNYERARRPGLLGASVLGLDDIHRAWRTFVLRVRAQDPPPELYFVKVDVTGAYDTI 720
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        661 LFSVLNYERARRPGLLGASVLGLDDIHRAWRTFVLRVRAQDPPPELYFVKVDVTGAYDTI 720

Qy        721 PQDRLTEVIASIIKPQNTYCVRRYAVVQKAAHGHVRKAFKSHVSTLTDLQPYMRQFVAHL 780
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        721 PQDRLTEVIASIIKPQNTYCVRRYAVVQKAAHGHVRKAFKSHVSTLTDLQPYMRQFVAHL 780

Qy        781 QETSPLRDAVVIEQSSSLNEASSGLFDVFLRFMCHHAVRIRGKSYVQCQGIPQGSILSTL 840
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        781 QETSPLRDAVVIEQSSSLNEASSGLFDVFLRFMCHHAVRIRGKSYVQCQGIPQGSILSTL 840

Qy        841 LCSLCYGDMENKLFAGIRRDGLLLRLVDDFLLVTPHLTHAKTFLRTLVRGVPEYGCVVNL 900
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        841 LCSLCYGDMENKLFAGIRRDGLLLRLVDDFLLVTPHLTHAKTFLRTLVRGVPEYGCVVNL 900

Qy        901 RKTVVNFPVEDEALGGTAFVQMPAHGLFPWCGLLLDTRTLEVQSDYSSYARTSIRASLTF 960
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        901 RKTVVNFPVEDEALGGTAFVQMPAHGLFPWCGLLLDTRTLEVQSDYSSYARTSIRASLTF 960

Qy        961 NRGFKAGRNMRRKLFGVLRLKCHSLFLDLQVNSLQTVCTNIYKILLLQAYRFHACVLQLP 1020
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        961 NRGFKAGRNMRRKLFGVLRLKCHSLFLDLQVNSLQTVCTNIYKILLLQAYRFHACVLQLP 1020

Qy       1021 FHQQVWKNPTFFLRVISDTASLCYSILKAKNAGMSLGAKGAAGPLPSEAVQWLCHQAFLL 1080
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1021 FHQQVWKNPTFFLRVISDTASLCYSILKAKNAGMSLGAKGAAGPLPSEAVQWLCHQAFLL 1080

Qy       1081 KLTRHRVTYVPLLGSLRTAQTQLSRKLPGTTLTALEAAANPALPSDFKTILD 1132
              ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1081 KLTRHRVTYVPLLGSLRTAQTQLSRKLPGTTLTALEAAANPALPSDFKTILD 1132
```

RESULT 29
AAY96566
ID AAY96566 standard; protein; 1132 AA.

```
XX
AC   AAY96566;
XX
DT   12-SEP-2000  (first entry)
XX
DE   hEST2, a human telomerase catalytic subunit homologue.
XX
KW   hEST2; telomerase; catalytic subunit; reverse transcriptase; life-span;
KW   retinoblastoma; p53; tumour suppressor; inhibitor; arteriosclerosis;
KW   proliferation; immortal; tumour therapy; macular degeneration;
KW   activator. INK4.
XX
OS   Homo sapiens.
XX
PN   WO200031238-A2.
XX
PD   02-JUN-2000.
XX
PF   24-NOV-1999;   99WO-US027907.
XX
PR   25-NOV-1998;   98US-0109891P.
PR   17-FEB-1999;   99US-0120549P.
XX
PA   (GENE-) GENETICA INC.
XX
PI   Hannon GJ,  Beach DH;
XX
DR   WPI; 2000-400055/34.
DR   N-PSDB; AAA29388.
XX
PT   New method for increasing the proliferative capacity of cell lines
PT   comprises administering agents reversibly activating telomerase activity
PT   and reversibly inactivating Rb/INk4 and/or p53 pathways useful in
PT   treating age related diseases.
XX
PS   Claim 14; Page 116-119; 123pp; English.
XX
CC   This protein, designated hEST2, is a human telomerase catalytic subunit
CC   homologue of yeast EST2p and Euplotes p123. hEST2 is a member of the
CC   reverse transcriptase family of enzymes. The invention concerns methods
CC   and reagents for extending the life-span, e.g. the number of mitotic
CC   divisions, of a cell. The method relies on activation of a telomerase
CC   activity and inhibition of one or both of a retinoblastoma (Rb)/INK4
CC   pathway or a p53 pathway. Phosphorylation of Rb by cyclin-dependent
CC   kinases, cdk4 and cdk6, releases the cells into the division cycle.
CC   Binding of INK4 family members, e.g. the tumour suppressor p16INK4a,
CC   inhibits kinase activity and results in growth arrest. Rb inactivators
CC   can selectively and reversibly inactivate an Rb/INK4 pathway, especially
CC   an Rb/p16INK4a pathway. The oncoprotein MDM2 is a cellular inhibitor of
CC   Rb/E2F function and the p53 tumour suppressor and can also be used in the
CC   methods. Other molecules which can be used include cdk4 or cdk6 mutants.
CC   In particular, a cdk4 mutant is one which differs from at one or more of
CC   residues K22, R24, H95 and/or D97. Additional constructs include a
CC   papilloma virus E7 protein, or other viral oncoprotein which bypasses Rb
CC   and/or p53. Antisense constructs of the Rb and p16INK4a genes may also be
CC   used. The methods are useful for increasing the proliferative capacity of
CC   cells. The cells are subsequently of use in pharmaceutical and cosmetic
CC   preparations used to treat conditions related to (premature) ageing, e.g.
CC   macular degeneration and arteriosclerosis. The cells can also be used to
CC   replace tumour cell lines in vitro and for studies on biochemical and
CC   physiological aspects of growth and differentiation. Long lived
CC   (immortal) cells could also be of use in the production of normal or
CC   genetically engineered biotechnology products
XX
SQ   Sequence 1132 AA;

  Query Match             99.9%;  Score 5954;  DB 3;  Length 1132;
  Best Local Similarity   99.9%;  Pred. No. 0;
  Matches 1131;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          1 MPRAPRCRAVRSLLRSHYREVLPLATFVRRLGPQGWRLVQRGDPAAFRALVAQCLVCVPW 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 MPRAPRCRAVRSLLRSHYREVLPLATFVRRLGPQGWRLVQRGDPAAFRALVAQCLVCVPW 60

Qy         61 DARPPPAAPSFRQVSCLKELVARVLQRLCERGAKNVLAFGFALLDGARGGPPEAFTTSVR 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 DARPPPAAPSFRQVSCLKELVARVLQRLCERGAKNVLAFGFALLDGARGGPPEAFTTSVR 120

Qy        121 SYLPNTVTDALRGSGAWGLLLRRVGDDVLVHLLARCALFVLVAPSCAYQVCGPPLYQLGA 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 SYLPNTVTDALRGSGAWGLLLRRVGDDVLVHLLARCALFVLVAPSCAYQVCGPPLYQLGA 180

Qy        181 ATQARPPPHASGPRRRLGCERAWNHSVREAGVPLGLPAPGARRRGGSASRSLPLPKRPRR 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 ATQARPPPHASGPRRRLGCERAWNHSVREAGVPLGLPAPGARRRGGSASRSLPLPKRPRR 240

Qy        241 GAAPEPERTPVGQGSWAHPGRTRGPSDRGFCVVSPARPAEEATSLEGALSGTRHSHPSVG 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 GAAPEPERTPVGQGSWAHPGRTRGPSDRGFCVVSPARPAEEATSLEGALSGTRHSHPSVG 300

Qy        301 RQHHAGPPSTSRPPRPWDTPCPPVYAETKHFLYSSGDKEQLRPSFLLSSLRPSLTGARRL 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 RQHHAGPPSTSRPPRPWDTPCPPVYAETKHFLYSSGDKEQLRPSFLLSSLRPSLTGARRL 360

Qy        361 VETIFLGSRPWMPGTPRRLPRLPQRYWQMRPLFLELLGNHAQCPYGVLLKTHCPLRAAVT 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        361 VETIFLGSRPWMPGTPRRLPRLPQRYWQMRPLFLELLGNHAQCPYGVLLKTHCPLRAAVT 420

Qy        421 PAAGVCAREKPQGSVAAPEEEDTDPRRLVQLLRQHSSPWQVYGFVRACLRRLVPPGLWGS 480
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        421 PAAGVCAREKPQGSVAAPEEEDTDPRRLVQLLRQHSSPWQVYGFVRACLRRLVPPGLWGS 480

Qy        481 RHNERRFLRNTKKFISLGKHAKLSLQELTWKMSVRDCAWLRRSPGVGCVPAAEHRLREEI 540
              |||||||||||||||||||||||||||||| ||||||||||||||||||||||||||||
Db        481 RHNERRFLRNTKKFISLGKHAKLSLQELTWKMSVRGCAWLRRSPGVGCVPAAEHRLREEI 540

Qy        541 LAKFLHWLMSVYVVELLRSFFYVTETTFQKNRLFFYRKSVWSKLQSIGIRQHLKRVQLRE 600
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        541 LAKFLHWLMSVYVVELLRSFFYVTETTFQKNRLFFYRKSVWSKLQSIGIRQHLKRVQLRE 600

Qy        601 LSEAEVRQHREARPALLTSRLRFIPKPDGLRPIVNMDYVVGARTFRREKRAERLTSRVKA 660
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        601 LSEAEVRQHREARPALLTSRLRFIPKPDGLRPIVNMDYVVGARTFRREKRAERLTSRVKA 660

Qy        661 LFSVLNYERARRPGLLGASVLGLDDIHRAWRTFVLRVRAQDPPPELYFVKVDVTGAYDTI 720
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        661 LFSVLNYERARRPGLLGASVLGLDDIHRAWRTFVLRVRAQDPPPELYFVKVDVTGAYDTI 720

Qy        721 PQDRLTEVIASIIKPQNTYCVRRYAVVQKAAHGHVRKAFKSHVSTLTDLQPYMRQFVAHL 780
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        721 PQDRLTEVIASIIKPQNTYCVRRYAVVQKAAHGHVRKAFKSHVSTLTDLQPYMRQFVAHL 780

Qy        781 QETSPLRDAVVIEQSSSLNEASSGLFDVFLRFMCHHAVRIRGKSYVQCQGIPQGSILSTL 840
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        781 QETSPLRDAVVIEQSSSLNEASSGLFDVFLRFMCHHAVRIRGKSYVQCQGIPQGSILSTL 840

Qy        841 LCSLCYGDMENKLFAGIRRDGLLLRLVDDFLLVTPHLTHAKTFLRTLVRGVPEYGCVVNL 900
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        841 LCSLCYGDMENKLFAGIRRDGLLLRLVDDFLLVTPHLTHAKTFLRTLVRGVPEYGCVVNL 900

Qy        901 RKTVVNFPVEDEALGGTAFVQMPAHGLFPWCGLLLDTRTLEVQSDYSSYARTSIRASLTF 960
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        901 RKTVVNFPVEDEALGGTAFVQMPAHGLFPWCGLLLDTRTLEVQSDYSSYARTSIRASLTF 960

Qy        961 NRGFKAGRNMRRKLFGVLRLKCHSLFLDLQVNSLQTVCTNIYKILLLQAYRFHACVLQLP 1020
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        961 NRGFKAGRNMRRKLFGVLRLKCHSLFLDLQVNSLQTVCTNIYKILLLQAYRFHACVLQLP 1020

Qy       1021 FHQQVWKNPTFFLRVISDTASLCYSILKAKNAGMSLGAKGAAGPLPSEAVQWLCHQAFLL 1080
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1021 FHQQVWKNPTFFLRVISDTASLCYSILKAKNAGMSLGAKGAAGPLPSEAVQWLCHQAFLL 1080

Qy       1081 KLTRHRVTYVPLLGSLRTAQTQLSRKLPGTTLTALEAAANPALPSDFKTILD 1132
              ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1081 KLTRHRVTYVPLLGSLRTAQTQLSRKLPGTTLTALEAAANPALPSDFKTILD 1132
```

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RESULT 30
ADC47061
ID   ADC47061 standard; protein; 1132 AA.
XX
AC   ADC47061;
XX
DT   18-DEC-2003  (first entry)
XX
DE   Human TERT amino acid sequence #SEQ ID 2.
XX
KW   Human; TERT; telomerase; antibody; reverse transcriptase; tumour;
KW   autoimmune disease; liver cancer.
XX
OS   Homo sapiens.
XX
PN   WO2003054545-A1.
XX
PD   03-JUL-2003.
XX
PF   19-DEC-2002; 2002WO-JP013310.
XX
PR   21-DEC-2001; 2001JP-00390050.
XX
PA   (MITS-) MITSUBISHI KAGAKU MEDICAL INC.
PA   (MURA/) MURAKAMI S.
PA   (KANE/) KANEKO S.
XX
PI   Murakami S,  Kaneko S,  Masutomi K;
XX
DR   WPI; 2003-569289/53.
DR   N-PSDB; ADC47060.
XX
PT   Detecting anti-telomerase antibody for detecting tumors and autoimmune
PT   disease.
XX
PS   Example Examples; Page 36-41; 45pp; Japanese.
XX
CC   The invention relates to a method for detecting an anti-telomerase
CC   antibody. The method of the invention comprises reacting telomerase
CC   producing protein and a fragment or complex of template RNA with anti-
CC   telomerase antibody in a sample, and analysing the product. The
CC   telomerase producing protein is preferably telomerase reverse
CC   transcriptase, and the analysis method is preferably western blot. The
CC   method can be used to detect for tumours and autoimmune disease. The
CC   method can also be used for detecting liver cancer. The current sequence
CC   represents the human TERT amino acid sequence.
XX
SQ   Sequence 1132 AA;

  Query Match             99.9%;  Score 5954;  DB 7;  Length 1132;
  Best Local Similarity   99.9%;  Pred. No. 0;
  Matches 1131;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          1 MPRAPRCRAVRSLLRSHYREVLPLATFVRRLGPQGWRLVQRGDPAAFRALVAQCLVCVPW 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 MPRAPRCRAVRSLLRSHYREVLPLATFVRRLGPQGWRLVQRGDPAAFRALVAQCLVCVPW 60

Qy         61 DARPPPAAPSFRQVSCLKELVARVLQRLCERGAKNVLAFGFALLDGARGGPPEAFTTSVR 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 DARPPPAAPSFRQVSCLKELVARVLQRLCERGAKNVLAFGFALLDGARGGPPEAFTTSVR 120

Qy        121 SYLPNTVTDALRGSGAWGLLLRRVGDDVLVHLLARCALFVLVAPSCAYQVCGPPLYQLGA 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 SYLPNTVTDALRGSGAWGLLLRRVGDDVLVHLLARCALFVLVAPSCAYQVCGPPLYQLGA 180

Qy        181 ATQARPPPHASGPRRRLGCERAWNHSVREAGVPLGLPAPGARRRGGSASRSLPLPKRPRR 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 ATQARPPPHASGPRRRLGCERAWNHSVREAGVPLGLPAPGARRRGGSASRSLPLPKRPRR 240

Qy        241 GAAPEPERTPVGQGSWAHPGRTRGPSDRGFCVVSPARPAEEATSLEGALSGTRHSHPSVG 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 GAAPEPERTPVGQGSWAHPGRTRGPSDRGFCVVSPARPAEEATSLEGALSGTRHSHPSVG 300

Qy        301 RQHHAGPPSTSRPPRPWDTPCPPVYAETKHFLYSSGDKEQLRPSFLLSSLRPSLTGARRL 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 RQHHAGPPSTSRPPRPWDTPCPPVYAETKHFLYSSGDKEQLRPSFLLSSLRPSLTGARRL 360

Qy        361 VETIFLGSRPWMPGTPRRLPRLPQRYWQMRPLFLELLGNHAQCPYGVLLKTHCPLRAAVT 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        361 VETIFLGSRPWMPGTPRRLPRLPQRYWQMRPLFLELLGNHAQCPYGVLLKTHCPLRAAVT 420

Qy        421 PAAGVCAREKPQGSVAAPEEEDTDPRRLVQLLRQHSSPWQVYGFVRACLRRLVPPGLWGS 480
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        421 PAAGVCAREKPQGSVAAPEEEDTDPRRLVQLLRQHSSPWQVYGFVRACLRRLVPPGLWGS 480

Qy        481 RHNERRFLRNTKKFISLGKHAKLSLQELTWKMSVRDCAWLRRSPGVGCVPAAEHRLREEI 540
              ||||||||||||||||||||||||||||||||| ||||||||||||||||||||||||||
Db        481 RHNERRFLRNTKKFISLGKHAKLSLQELTWKMSVRGCAWLRRSPGVGCVPAAEHRLREEI 540

Qy        541 LAKFLHWLMSVYVVELLRSFFYVTETTFQKNRLFFYRKSVWSKLQSIGIRQHLKRVQLRE 600
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        541 LAKFLHWLMSVYVVELLRSFFYVTETTFQKNRLFFYRKSVWSKLQSIGIRQHLKRVQLRE 600

Qy        601 LSEAEVRQHREARPALLTSRLRFIPKPDGLRPIVNMDYVVGARTFRREKRAERLTSRVKA 660
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        601 LSEAEVRQHREARPALLTSRLRFIPKPDGLRPIVNMDYVVGARTFRREKRAERLTSRVKA 660

Qy        661 LFSVLNYERARRPGLLGASVLGLDDIHRAWRTFVLRVRAQDPPPELYFVKVDVTGAYDTI 720
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        661 LFSVLNYERARRPGLLGASVLGLDDIHRAWRTFVLRVRAQDPPPELYFVKVDVTGAYDTI 720

Qy        721 PQDRLTEVIASIIKPQNTYCVRRYAVVQKAAHGHVRKAFKSHVSTLTDLQPYMRQFVAHL 780
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        721 PQDRLTEVIASIIKPQNTYCVRRYAVVQKAAHGHVRKAFKSHVSTLTDLQPYMRQFVAHL 780

Qy        781 QETSPLRDAVVIEQSSSLNEASSGLFDVFLRFMCHHAVRIRGKSYVQCQGIPQGSILSTL 840
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        781 QETSPLRDAVVIEQSSSLNEASSGLFDVFLRFMCHHAVRIRGKSYVQCQGIPQGSILSTL 840

Qy        841 LCSLCYGDMENKLFAGIRRDGLLLRLVDDFLLVTPHLTHAKTFLRTLVRGVPEYGCVVNL 900
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        841 LCSLCYGDMENKLFAGIRRDGLLLRLVDDFLLVTPHLTHAKTFLRTLVRGVPEYGCVVNL 900

Qy        901 RKTVVNFPVEDEALGGTAFVQMPAHGLFPWCGLLLDTRTLEVQSDYSSYARTSIRASLTF 960
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        901 RKTVVNFPVEDEALGGTAFVQMPAHGLFPWCGLLLDTRTLEVQSDYSSYARTSIRASLTF 960

Qy        961 NRGFKAGRNMRRKLFGVLRLKCHSLFLDLQVNSLQTVCTNIYKILLLQAYRFHACVLQLP 1020
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        961 NRGFKAGRNMRRKLFGVLRLKCHSLFLDLQVNSLQTVCTNIYKILLLQAYRFHACVLQLP 1020

Qy       1021 FHQQVWKNPTFFLRVISDTASLCYSILKAKNAGMSLGAKGAAGPLPSEAVQWLCHQAFLL 1080
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1021 FHQQVWKNPTFFLRVISDTASLCYSILKAKNAGMSLGAKGAAGPLPSEAVQWLCHQAFLL 1080

Qy       1081 KLTRHRVTYVPLLGSLRTAQTQLSRKLPGTTLTALEAAANPALPSDFKTILD 1132
              ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1081 KLTRHRVTYVPLLGSLRTAQTQLSRKLPGTTLTALEAAANPALPSDFKTILD 1132


RESULT 31
ADE40482
ID   ADE40482 standard; protein; 1132 AA.
XX
AC   ADE40482;
XX
DT   29-JAN-2004  (first entry)
XX
DE   Human telomerase reverse transcriptase (hTERT).
XX
KW   Immortal porcine cell; telomerase reverse transcriptase; epithelial cell;
KW   uterine endometrial glandular tissue; virus quantification;
KW   virus production; porcine reproductive and respiratory syndrome virus;
KW   PRRSV; toxicity evaluation; human; hTERT; enzyme.
XX
```

OS Homo sapiens.
XX
PN WO2003077853-A2.
XX
PD 25-SEP-2003.
XX
PF 11-MAR-2003; 2003WO-US007526.
XX
PR 11-MAR-2002; 2002US-0363129P.
XX
PA (MINU) UNIV MINNESOTA.
XX
PI Farris JA, Foster DN, O'grady SM;
XX
DR WPI; 2003-779075/73.
DR N-PSDB; ADE40481.
XX
PT New immortal porcine cell comprising a polynucleotide encoding an
PT exogenous telomerase reverse transcriptase polypeptide, useful for
PT measuring the amount of virus in a sample or for evaluating toxicity of a
PT compound.
XX
PS Claim 4; SEQ ID NO 2; 42pp; English.
XX
CC The invention relates to immortal porcine cells comprising a
CC polynucleotide encoding an exogenous telomerase reverse transcriptase
CC (TERT). The invention also encompasses the method of making immortal
CC porcine cells, and the use of the immortal porcine cells for measuring
CC the amount of virus in a sample, producing a virus, and evaluating the
CC toxicity of a compound. The cells of the invention may be diploid or
CC aneuploid, and may be an epithelial cell obtained from uterine
CC endometrial glandular tissue. The exogenous telomerase reverse
CC transcriptase expressed by the cells of the invention is preferably human
CC telomerase reverse transcriptase (ADE40482). The immortal porcine cells
CC are useful for measuring an amount of a virus in a sample, producing a
CC virus (especially porcine reproductive and respiratory syndrome virus
CC (PRRSV)), or for evaluating toxicity of a compound. The present sequence
CC represents human telomerase reverse transcriptase (hTERT), which is
CC claimed for use in the immortal cells of the invention.
XX
SQ Sequence 1132 AA;

Query Match 99.9%; Score 5954; DB 7; Length 1132;
Best Local Similarity 99.9%; Pred. No. 0;
Matches 1131; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

```
Qy          1 MPRAPRCRAVRSLLRSHYREVLPLATFVRRLGPQGWRLVQRGDPAAFRALVAQCLVCVPW 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 MPRAPRCRAVRSLLRSHYREVLPLATFVRRLGPQGWRLVQRGDPAAFRALVAQCLVCVPW 60

Qy         61 DARPPPAAPSFRQVSCLKELVARVLQRLCERGAKNVLAFGFALLDGARGGPPEAFTTSVR 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 DARPPPAAPSFRQVSCLKELVARVLQRLCERGAKNVLAFGFALLDGARGGPPEAFTTSVR 120

Qy        121 SYLPNTVTDALRGSGAWGLLLRRVGDDVLVHLLARCALFVLVAPSCAYQVCGPPLYQLGA 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 SYLPNTVTDALRGSGAWGLLLRRVGDDVLVHLLARCALFVLVAPSCAYQVCGPPLYQLGA 180

Qy        181 ATQARPPPHASGPRRRLGCERAWNHSVREAGVPLGLPAPGARRRGGSASRSLPLPKRPRR 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 ATQARPPPHASGPRRRLGCERAWNHSVREAGVPLGLPAPGARRRGGSASRSLPLPKRPRR 240

Qy        241 GAAPEPERTPVGQGSWAHPGRTRGPSDRGFCVVSPARPAEEATSLEGALSGTRHSHPSVG 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 GAAPEPERTPVGQGSWAHPGRTRGPSDRGFCVVSPARPAEEATSLEGALSGTRHSHPSVG 300

Qy        301 RQHHAGPPSTSRPPRPWDTPCPPVYAETKHFLYSSGDKEQLRPSFLLSSLRPSLTGARRL 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 RQHHAGPPSTSRPPRPWDTPCPPVYAETKHFLYSSGDKEQLRPSFLLSSLRPSLTGARRL 360

Qy        361 VETIFLGSRPWMPGTPRRLPRLPQRYWQMRPLFLELLGNHAQCPYGVLLKTHCPLRAAVT 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        361 VETIFLGSRPWMPGTPRRLPRLPQRYWQMRPLFLELLGNHAQCPYGVLLKTHCPLRAAVT 420

Qy        421 PAAGVCAREKPQGSVAAPEEEDTDPRRLVQLLRQHSSPWQVYGFVRACLRRLVPPGLWGS 480
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        421 PAAGVCAREKPQGSVAAPEEEDTDPRRLVQLLRQHSSPWQVYGFVRACLRRLVPPGLWGS 480

Qy        481 RHNERRFLRNTKKFISLGKHAKLSLQELTWKMSVRDCAWLRRSPGVGCVPAAEHRLREEI 540
              ||||||||||||||||||||||||||||||||| ||||||||||||||||||||||||||
Db        481 RHNERRFLRNTKKFISLGKHAKLSLQELTWKMSVRGCAWLRRSPGVGCVPAAEHRLREEI 540

Qy        541 LAKFLHWLMSVYVVELLRSFFYVTETTFQKNRLFFYRKSVWSKLQSIGIRQHLKRVQLRE 600
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        541 LAKFLHWLMSVYVVELLRSFFYVTETTFQKNRLFFYRKSVWSKLQSIGIRQHLKRVQLRE 600

Qy        601 LSEAEVRQHREARPALLTSRLRFIPKPDGLRPIVNMDYVVGARTFRREKRAERLTSRVKA 660
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        601 LSEAEVRQHREARPALLTSRLRFIPKPDGLRPIVNMDYVVGARTFRREKRAERLTSRVKA 660

Qy        661 LFSVLNYERARRPGLLGASVLGLDDIHRAWRTFVLRVRAQDPPPELYFVKVDVTGAYDTI 720
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        661 LFSVLNYERARRPGLLGASVLGLDDIHRAWRTFVLRVRAQDPPPELYFVKVDVTGAYDTI 720

Qy        721 PQDRLTEVIASIIKPQNTYCVRRYAVVQKAAHGHVRKAFKSHVSTLTDLQPYMRQFVAHL 780
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        721 PQDRLTEVIASIIKPQNTYCVRRYAVVQKAAHGHVRKAFKSHVSTLTDLQPYMRQFVAHL 780

Qy        781 QETSPLRDAVVIEQSSSLNEASSGLFDVFLRFMCHHAVRIRGKSYVQCQGIPQGSILSTL 840
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        781 QETSPLRDAVVIEQSSSLNEASSGLFDVFLRFMCHHAVRIRGKSYVQCQGIPQGSILSTL 840

Qy        841 LCSLCYGDMENKLFAGIRRDGLLLRLVDDFLLVTPHLTHAKTFLRTLVRGVPEYGCVVNL 900
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        841 LCSLCYGDMENKLFAGIRRDGLLLRLVDDFLLVTPHLTHAKTFLRTLVRGVPEYGCVVNL 900

Qy        901 RKTVVNFPVEDEALGGTAFVQMPAHGLFPWCGLLLDTRTLEVQSDYSSYARTSIRASLTF 960
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        901 RKTVVNFPVEDEALGGTAFVQMPAHGLFPWCGLLLDTRTLEVQSDYSSYARTSIRASLTF 960

Qy        961 NRGFKAGRNMRRKLFGVLRLKCHSLFLDLQVNSLQTVCTNIYKILLLQAYRFHACVLQLP 1020
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        961 NRGFKAGRNMRRKLFGVLRLKCHSLFLDLQVNSLQTVCTNIYKILLLQAYRFHACVLQLP 1020

Qy       1021 FHQQVWKNPTFFLRVISDTASLCYSILKAKNAGMSLGAKGAAGPLPSEAVQWLCHQAFLL 1080
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1021 FHQQVWKNPTFFLRVISDTASLCYSILKAKNAGMSLGAKGAAGPLPSEAVQWLCHQAFLL 1080

Qy       1081 KLTRHRVTYVPLLGSLRTAQTQLSRKLPGTTLTALEAAANPALPSDFKTILD 1132
              ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1081 KLTRHRVTYVPLLGSLRTAQTQLSRKLPGTTLTALEAAANPALPSDFKTILD 1132
```

RESULT 32
AAW56113
ID AAW56113 standard; protein; 1132 AA.
XX
AC AAW56113;
XX
DT 13-AUG-1998 (first entry)
XX
DE Human telomerase reverse transcriptase protein refined sequence.
XX
KW Human; telomerase reverse transcriptase; hTRT; TRT; diagnosis; prognosis;
KW cell proliferation; cancer; ageing; ribonucleoprotein.
XX
OS Homo sapiens.
XX
PN GB2317891-A.
XX
PD 08-APR-1998.
XX
PF 01-OCT-1997; 97GB-00020890.
XX
PR 01-OCT-1996; 96US-00724643.
PR 18-APR-1997; 97US-00844419.

```
PR   25-APR-1997;   97US-00846017.
PR   06-MAY-1997;   97US-00851843.
PR   09-MAY-1997;   97US-00854050.
PR   14-AUG-1997;   97US-00911312.
PR   14-AUG-1997;   97US-00912951.
PR   14-AUG-1997;   97US-00915503.
XX
PA   (GERO-) GERON CORP.
PA   (UYTE-) UNIV TECHNOLOGY CORP.
XX
PI   Cech TR, Lingner J, Nakamura T, Chapman KB, Morin GB, Harley CB;
PI   Andrews WH;
XX
DR   WPI; 1998-171633/16.
DR   N-PSDB; AAV22428.
XX
PT   Pure and recombinant human Telomerase Reverse Transcriptase and its
PT   variants - are useful in the diagnosis, prognosis and treatment of cell
PT   proliferation conditions especially cancer and ageing.
XX
PS   Example 1; Fig 74; 387pp; English.
XX
CC   The present sequence represents human telomerase reverse transcriptase
CC   (hTRT), which is a ribonucleoprotein. The present invention also
CC   describes the following methods: (A) determining whether a test compound
CC   is a modulator of hTRT, by detecting the change in hTRT recombinant
CC   protein or polynucleotide, on administration of the compound; (B)
CC   preparation of recombinant telomerase by contacting a protein preparation
CC   of hTRT with a telomerase RNA component; (C) detection of the hTRT RNA or
CC   protein in a sample by binding a relevant probe to the sample and
CC   detecting the complex formed or in the case of RNA detection, amplifying
CC   the product and correlating the presence of complex or amplification
CC   product with presence of hTRT in the sample; and (D) increasing the
CC   proliferation of a vertebrate cell by increasing hTRT expression; and (E)
CC   the use of an agent that causes an increase in cell vertebrate cell
CC   proliferation to create a medicament that inhibits ageing. A protein
CC   preparation of hTRT and the polynucleotide encoding hTRT can be used in
CC   the manufacture of medicaments for inhibiting the effect of ageing or
CC   cancer. Inhibitors of telomerase activity can be used to treat conditions
CC   that are associated with high telomerase activity. A protein preparation
CC   of hTRT can also be used in the new methods
XX
SQ   Sequence 1132 AA;

  Query Match            99.8%;  Score 5952;  DB 2;  Length 1132;
  Best Local Similarity  99.8%;  Pred. No. 0;
  Matches 1130;  Conservative    1;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          1 MPRAPRCRAVRSLLRSHYREVLPLATFVRRLGPQGWRLVQRGDPAAFRALVAQCLVCVPW 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 MPRAPRCRAVRSLLRSHYREVLPLATFVRRLGPQGWRLVQRGDPAAFRALVAQCLVCVPW 60

Qy         61 DARPPPAAPSFRQVSCLKELVARVLQRLCERGAKNVLAFGFALLDGARGGPPEAFTTSVR 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 DARPPPAAPSFRQVSCLKELVARVLQRLCERGAKNVLAFGFALLDGARGGPPEAFTTSVR 120

Qy        121 SYLPNTVTDALRGSGAWGLLLRRVGDDVLVHLLARCALFVLVAPSCAYQVCGPPLYQLGA 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 SYLPNTVTDALRGSGAWGLLLRRVGDDVLVHLLARCALFVLVAPSCAYQVCGPPLYQLGA 180

Qy        181 ATQARPPPHASGPRRRLGCERAWNHSVREAGVPLGLPAPGARRRGGSASRSLPLPKRPRR 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 ATQARPPPHASGPRRRLGCERAWNHSVREAGVPLGLPAPGARRRGGSASRSLPLPKRPRR 240

Qy        241 GAAPEPERTPVGQGSWAHPGRTRGPSDRGFCVVSPARPAEEATSLEGALSGTRHSHPSVG 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 GAAPEPERTPVGQGSWAHPGRTRGPSDRGFCVVSPARPAEEATSLEGALSGTRHSHPSVG 300

Qy        301 RQHHAGPPSTSRPPRPWDTPCPPVYAETKHFLYSSGDKEQLRPSFLLSSLRPSLTGARRL 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 RQHHAGPPSTSRPPRPWDTPCPPVYAETKHFLYSSGDKEQLRPSFLLSSLRPSLTGARRL 360

Qy        361 VETIFLGSRPWMPGTPRRLPRLPQRYWQMRPLFLELLGNHAQCPYGVLLKTHCPLRAAVT 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        361 VETIFLGSRPWMPGTPRRLPRLPQRYWQMRPLFLELLGNHAQCPYGVLLKTHCPLRAAVT 420

Qy        421 PAAGVCAREKPQGSVAAPEEEDTDPRRLVQLLRQHSSPWQVYGFVRACLRRLVPPGLWGS 480
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        421 PAAGVCAREKPQGSVAAPEEEDTDPRRLVQLLRQHSSPWQVYGFVRACLRRLVPPGLWGS 480

Qy        481 RHNERRFLRNTKKFISLGKHAKLSLQELTWKMSVRDCAWLRRSPGVGCVPAAEHRLREEI 540
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        481 RHNERRFLRNTKKFISLGKHAKLSLQELTWKMSVRDCAWLRRSPGVGCVPAAEHRLREEI 540

Qy        541 LAKFLHWLMSVYVVELLRSFFYVTETTFQKNRLFFYRKSVWSKLQSIGIRQHLKRVQLRE 600
              |||||||||||||||||||||||||||||||| ||||||||||||||||||||||||||
Db        541 LAKFLHWLMSVYVVELLRSFFYVTETTFQKNRLFFYRPSVWSKLQSIGIRQHLKRVQLRE 600

Qy        601 LSEAEVRQHREARPALLTSRLRFIPKPDGLRPIVNMDYVVGARTFRREKRAERLTSRVKA 660
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        601 LSEAEVRQHREARPALLTSRLRFIPKPDGLRPIVNMDYVVGARTFRREKRAERLTSRVKA 660

Qy        661 LFSVLNYERARRPGLLGASVLGLDDIHRAWRTFVLRVRAQDPPPELYFVKVDVTGAYDTI 720
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        661 LFSVLNYERARRPGLLGASVLGLDDIHRAWRTFVLRVRAQDPPPELYFVKVDVTGAYDTI 720

Qy        721 PQDRLTEVIASIIKPQNTYCVRRYAVVQKAAHGHVRKAFKSHVSTLTDLQPYMRQFVAHL 780
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        721 PQDRLTEVIASIIKPQNTYCVRRYAVVQKAAHGHVRKAFKSHVSTLTDLQPYMRQFVAHL 780

Qy        781 QETSPLRDAVVIEQSSSLNEASSGLFDVFLRFMCHHAVRIRGKSYVQCQGIPQGSILSTL 840
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        781 QETSPLRDAVVIEQSSSLNEASSGLFDVFLRFMCHHAVRIRGKSYVQCQGIPQGSILSTL 840

Qy        841 LCSLCYGDMENKLFAGIRRDGLLLRLVDDFLLVTPHLTHAKTFLRTLVRGVPEYGCVVNL 900
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        841 LCSLCYGDMENKLFAGIRRDGLLLRLVDDFLLVTPHLTHAKTFLRTLVRGVPEYGCVVNL 900

Qy        901 RKTVVNFPVEDEALGGTAFVQMPAHGLFPWCGLLLDTRTLEVQSDYSSYARTSIRASLTF 960
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||:||
Db        901 RKTVVNFPVEDEALGGTAFVQMPAHGLFPWCGLLLDTRTLEVQSDYSSYARTSIRASVTF 960

Qy        961 NRGFKAGRNMRRKLFGVLRLKCHSLFLDLQVNSLQTVCTNIYKILLLQAYRFHACVLQLP 1020
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        961 NRGFKAGRNMRRKLFGVLRLKCHSLFLDLQVNSLQTVCTNIYKILLLQAYRFHACVLQLP 1020

Qy       1021 FHQQVWKNPTFFLRVISDTASLCYSILKAKNAGMSLGAKGAAGPLPSEAVQWLCHQAFLL 1080
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1021 FHQQVWKNPTFFLRVISDTASLCYSILKAKNAGMSLGAKGAAGPLPSEAVQWLCHQAFLL 1080

Qy       1081 KLTRHRVTYVPLLGSLRTAQTQLSRKLPGTTLTALEAAANPALPSDFKTILD 1132
              ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1081 KLTRHRVTYVPLLGSLRTAQTQLSRKLPGTTLTALEAAANPALPSDFKTILD 1132


RESULT 33
AAY00647
ID   AAY00647 standard; protein; 1166 AA.
XX
AC   AAY00647;
XX
DT   26-JUL-1999  (first entry)
XX
DE   Telomerase (ver. 2) protein sequence.
XX
KW   Telomerase; human; cancer; diagnosis; melanoma; skin cancer; leukaemia;
KW   neuroblastoma; breast carcinoma; colon carcinoma; lymphoma; osteosarcoma;
KW   smooth muscle cell hyperplasia; stem cell proliferation; Wilm's tumour;
KW   stem cell differentiation; organ regeneration; organ differentiation.
XX
OS   Homo sapiens.
OS   Synthetic.
XX
PN   WO9901560-A1.
XX
PD   14-JAN-1999.
```

```
XX
PF   01-JUL-1998;   98WO-US013835.
XX
PR   01-JUL-1997;   97US-0051410P.
PR   21-JUL-1997;   97US-0053018P.
PR   21-JUL-1997;   97US-0053329P.
PR   04-AUG-1997;   97US-0054642P.
PR   09-SEP-1997;   97US-0058287P.
XX
PA   (CAMB-) CAMBIA BIOSYSTEMS LLC.
XX
PI   Kilian A,  Bowtell D;
XX
DR   WPI; 1999-106060/09.
DR   N-PSDB; AAX18275.
XX
PT   New isolated vertebrate telomerase genes - used to develop products for
PT   treating cancers or for organ regeneration, nerve cell or brain cell
PT   growth following injury or bone marrow transplantation.
XX
PS   Claim 4; Fig 11z-ac; 134pp; English.
XX
CC   This sequence is a truncated human telomerase of the invention. Primers
CC   that amplify the telomerase coding sequence can be used in a method for
CC   diagnosing cancer in a patient. The telomerase can be used for detection,
CC   diagnosis and drug screening. Inhibitors of telomerase activity can be
CC   used to treat cancers such as melanomas, other skin cancers,
CC   neuroblastomas, breast carcinomas, colon carcinomas, leukaemias,
CC   lymphomas, osteosarcomas or smooth muscle cell hyperplasias or skin
CC   growths. Enhancers of telomerase may be used to stimulate stem cell
CC   proliferation and differentiation (expansion of haematopoietic stem cells
CC   could be administered in the bone marrow transplant context). As well,
CC   many tissues have stem cells. Proliferation of these cells may be useful
CC   in wound healing, hair growth, treatment of disease such as Wilm's
CC   tumour, organ regeneration or differentiation after injury or diseases,
CC   nerve cell or brain cell growth following injury
XX
SQ   Sequence 1166 AA;

  Query Match             99.4%;  Score 5927;  DB 2;  Length 1166;
  Best Local Similarity   97.0%;  Pred. No. 0;
  Matches 1131;  Conservative    0;  Mismatches    1;  Indels   34;  Gaps    1;

Qy          1 MPRAPRCRAVRSLLRSHYREVLPLATFVRRLGPQGWRLVQRGDPAAFRALVAQCLVCVPW 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 MPRAPRCRAVRSLLRSHYREVLPLATFVRRLGPQGWRLVQRGDPAAFRALVAQCLVCVPW 60

Qy         61 DARPPPAAPSFRQV----------------------------------SCLKELVARVLQ 86
              |||||||||||||                                  ||||||||||||
Db         61 DARPPPAAPSFRQVGLPGVGVRLGLRAAGGNQRHAESSAGDSGRFPRRSCLKELVARVLQ 120

Qy         87 RLCERGAKNVLAFGFALLDGARGGPPEAFTTSVRSYLPNTVTDALRGSGAWGLLLRRVGD 146
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 RLCERGAKNVLAFGFALLDGARGGPPEAFTTSVRSYLPNTVTDALRGSGAWGLLLRRVGD 180

Qy        147 DVLVHLLARCALFVLVAPSCAYQVCGPPLYQLGAATQARPPPHASGPRRRLGCERAWNHS 206
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 DVLVHLLARCALFVLVAPSCAYQVCGPPLYQLGAATQARPPPHASGPRRRLGCERAWNHS 240

Qy        207 VREAGVPLGLPAPGARRRGGSASRSLPLPKRPRRGAAPEPERTPVGQGSWAHPGRTRGPS 266
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 VREAGVPLGLPAPGARRRGGSASRSLPLPKRPRRGAAPEPERTPVGQGSWAHPGRTRGPS 300

Qy        267 DRGFCVVSPARPAEEATSLEGALSGTRHSHPSVGRQHHAGPPSTSRPPRPWDTPCPPVYA 326
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 DRGFCVVSPARPAEEATSLEGALSGTRHSHPSVGRQHHAGPPSTSRPPRPWDTPCPPVYA 360

Qy        327 ETKHFLYSSGDKEQLRPSFLLSSLRPSLTGARRLVETIFLGSRPWMPGTPRRLPRLPQRY 386
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        361 ETKHFLYSSGDKEQLRPSFLLSSLRPSLTGARRLVETIFLGSRPWMPGTPRRLPRLPQRY 420

Qy        387 WQMRPLFLELLGNHAQCPYGVLLKTHCPLRAAVTPAAGVCAREKPQGSVAAPEEEDTDPR 446
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||

Db        421 WQMRPLFLELLGNHAQCPYGVLLKTHCPLRAAVTPAAGVCAREKPQGSVAAPEEEDTDPR 480

Qy        447 RLVQLLRQHSSPWQVYGFVRACLRRLVPPGLWGSRHNERRFLRNTKKFISLGKHAKLSLQ 506
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        481 RLVQLLRQHSSPWQVYGFVRACLRRLVPPGLWGSRHNERRFLRNTKKFISLGKHAKLSLQ 540

Qy        507 ELTWKMSVRDCAWLRRSPGVGCVPAAEHRLREEILAKFLHWLMSVYVVELLRSFFYVTET 566
              ||||||||| ||||||||||||||||||||||||||||||||||||||||||||||||||
Db        541 ELTWKMSVRGCAWLRRSPGVGCVPAAEHRLREEILAKFLHWLMSVYVVELLRSFFYVTET 600

Qy        567 TFQKNRLFFYRKSVWSKLQSIGIRQHLKRVQLRELSEAEVRQHREARPALLTSRLRFIPK 626
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        601 TFQKNRLFFYRKSVWSKLQSIGIRQHLKRVQLRELSEAEVRQHREARPALLTSRLRFIPK 660

Qy        627 PDGLRPIVNMDYVVGARTFRREKRAERLTSRVKALFSVLNYERARRPGLLGASVLGLDDI 686
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        661 PDGLRPIVNMDYVVGARTFRREKRAERLTSRVKALFSVLNYERARRPGLLGASVLGLDDI 720

Qy        687 HRAWRTFVLRVRAQDPPPELYFVKVDVTGAYDTIPQDRLTEVIASIIKPQNTYCVRRYAV 746
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        721 HRAWRTFVLRVRAQDPPPELYFVKVDVTGAYDTIPQDRLTEVIASIIKPQNTYCVRRYAV 780

Qy        747 VQKAAHGHVRKAFKSHVSTLTDLQPYMRQFVAHLQETSPLRDAVVIEQSSSLNEASSGLF 806
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        781 VQKAAHGHVRKAFKSHVSTLTDLQPYMRQFVAHLQETSPLRDAVVIEQSSSLNEASSGLF 840

Qy        807 DVFLRFMCHHAVRIRGKSYVQCQGIPQGSILSTLLCSLCYGDMENKLFAGIRRDGLLLRL 866
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        841 DVFLRFMCHHAVRIRGKSYVQCQGIPQGSILSTLLCSLCYGDMENKLFAGIRRDGLLLRL 900

Qy        867 VDDFLLVTPHLTHAKTFLRTLVRGVPEYGCVVNLRKTVVNFPVEDEALGGTAFVQMPAHG 926
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        901 VDDFLLVTPHLTHAKTFLRTLVRGVPEYGCVVNLRKTVVNFPVEDEALGGTAFVQMPAHG 960

Qy        927 LFPWCGLLLDTRTLEVQSDYSSYARTSIRASLTFNRGFKAGRNMRRKLFGVLRLKCHSLF 986
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        961 LFPWCGLLLDTRTLEVQSDYSSYARTSIRASLTFNRGFKAGRNMRRKLFGVLRLKCHSLF 1020

Qy        987 LDLQVNSLQTVCTNIYKILLLQAYRFHACVLQLPFHQQVWKNPTFFLRVISDTASLCYSI 1046
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1021 LDLQVNSLQTVCTNIYKILLLQAYRFHACVLQLPFHQQVWKNPTFFLRVISDTASLCYSI 1080

Qy       1047 LKAKNAGMSLGAKGAAGPLPSEAVQWLCHQAFLLKLTRHRVTYVPLLGSLRTAQTQLSRK 1106
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1081 LKAKNAGMSLGAKGAAGPLPSEAVQWLCHQAFLLKLTRHRVTYVPLLGSLRTAQTQLSRK 1140

Qy       1107 LPGTTLTALEAAANPALPSDFKTILD 1132
              |||||||||||||||||||||||||
Db       1141 LPGTTLTALEAAANPALPSDFKTILD 1166


RESULT 34
AAW56101
ID   AAW56101 standard; protein; 1405 AA.
XX
AC   AAW56101;
XX
DT   13-AUG-1998  (first entry)
XX
DE   Enhanced green fluorescent protein and hTRT fusion protein.
XX
KW   Human; telomerase reverse transcriptase; hTRT; TRT; diagnosis; prognosis;
KW   cell proliferation; cancer; ageing; ribonucleoprotein.
XX
OS   Synthetic.
OS   Homo sapiens.
XX
FH   Key             Location/Qualifiers
FT   Region          1. .250
FT                   /note= "enhanced green fluorescent protein fragment"
FT   Region          276. .1405
FT                   /note= "hTRT protein fragment"
XX
```

PN GB2317891-A.
XX
PD 08-APR-1998.
XX
PF 01-OCT-1997; 97GB-00020890.
XX
PR 01-OCT-1996; 96US-00724643.
PR 18-APR-1997; 97US-00844419.
PR 25-APR-1997; 97US-00846017.
PR 06-MAY-1997; 97US-00851843.
PR 09-MAY-1997; 97US-00854050.
PR 14-AUG-1997; 97US-00911312.
PR 14-AUG-1997; 97US-00912951.
PR 14-AUG-1997; 97US-00915503.
XX
PA (GERO-) GERON CORP.
PA (UYTE-) UNIV TECHNOLOGY CORP.
XX
PI Cech TR, Lingner J, Nakamura T, Chapman KB, Morin GB, Harley CB;
PI Andrews WH;
XX
DR WPI; 1998-171633/16.
XX
PT Pure and recombinant human Telomerase Reverse Transcriptase and its
PT variants - are useful in the diagnosis, prognosis and treatment of cell
PT proliferation conditions especially cancer and ageing.
XX
PS Example 15; Page 269-270; 387pp; English.
XX
CC The present sequence represents a fusion protein from an example of the
CC present invention which describes human telomerase reverse transcriptase
CC (hTRT). The present invention also describes the following methods: (A)
CC determining whether a test compound is a modulator of hTRT, by detecting
CC the change in hTRT recombinant protein or polynucleotide, on
CC administration of the compound; (B) preparation of recombinant telomerase
CC by contacting a protein preparation of hTRT with a telomerase RNA
CC component; (C) detection of the hTRT RNA or protein in a sample by
CC binding a relevant probe to the sample and detecting the complex formed
CC or in the case of RNA detection, amplifying the product and correlating
CC the presence of complex or amplification product with presence of hTRT in
CC the sample; and (D) increasing the proliferation of a vertebrate cell by
CC increasing hTRT expression; and (E) the use of an agent that causes an
CC increase in cell vertebrate cell proliferation to create a medicament
CC that inhibits ageing. A protein preparation of hTRT and the
CC polynucleotide encoding hTRT can be used in the manufacture of
CC medicaments for inhibiting the effect of ageing or cancer. Inhibitors of
CC telomerase activity can be used to treat conditions that are associated
CC with high telomerase activity. A protein preparation of hTRT can also be
CC used in the new methods
XX
SQ Sequence 1405 AA;

Query Match 99.3%; Score 5918; DB 2; Length 1405;
Best Local Similarity 99.6%; Pred. No. 0;
Matches 1128; Conservative 1; Mismatches 1; Indels 2; Gaps 2;

```
Qy          1 MPRAPRCRAVRSLLRSHYREVLPLATFVRRLGPQGWRLVQRGDPAAFRALVAQCLVCVPW 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        276 MPRAPRCRAVRSLLRSHYREVLPLATFVRRLGPQGWRLVQRGDPAAFRALVAQCLVCVPW 335

Qy         61 DARPPPAAPSFRQVSCLKELVARVLQRLCERGAKNVLAFGFALLDGARGGPPEAFTTSVR 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        336 DARPPPAAPSFRQVSCLKELVARVLQRLCERGAKNVLAFGFALLDGARGGPPEAFTTSVR 395

Qy        121 SYLPNTVTDALRGSGAWGLLLRRVGDDVLVHLLARCALFVLVAPSCAYQVCGPPLYQLGA 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        396 SYLPNTVTDALRGSGAWGLLLRRVGDDVLVHLLARCALFVLVAPSCAYQVCGPPLYQLGA 455

Qy        181 ATQARPPPHASGPRRRLGCERAWNHSVREAGVPLGLPAPGARRRGGSASRSLPLPKRPRR 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        456 ATQARPPPHASGPRRRLGCERAWNHSVREAGVPLGLPAPGARRRGGSASRSLPLPKRPRR 515

Qy        241 GAAPEPERTPVGQGSWAHPGRTRGPSDRGFCVVSPARPAEEATSLEGALSGTRHSHPSVG 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        516 GAAPEPERTPVGQGSWAHPGRTRGPSDRGFCVVSPARPAEEATSLEGALSGTRHSHPSVG 575

Qy        301 RQHHAGPPSTSRPPRPWDTPCPPVYAETKHFLYSSGDKEQLRPSFLLSSLRPSLTGARRL 360
              |||||||||||||||||||||||||||| ||||||||||||||||||||||||||||||
Db        576 RQHHAGPPSTSRPPRPWDTPCPPVYAETK-FLYSSGDKEQLRPSFLLSSLRPSLTGARRL 634

Qy        361 VETIFLGSRPWMPGTPRRLPRLPQRYWQMRPLFLELLGNHAQCPYGVLLKTHCPLRAAVT 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        635 VETIFLGSRPWMPGTPRRLPRLPQRYWQMRPLFLELLGNHAQCPYGVLLKTHCPLRAAVT 694

Qy        421 PAAGVCAREKPQGSVAAPEEEDTDPRRLVQLLRQHSSPWQVYGFVRACLRRLVPPGLWGS 480
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        695 PAAGVCAREKPQGSVAAPEEEDTDPRRLVQLLRQHSSPWQVYGFVRACLRRLVPPGLWGS 754

Qy        481 RHNERRFLRNTKKFISLGKHAKLSLQELTWKMSVRDCAWLRRSPGVGCVPAAEHRLREEI 540
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        755 RHNERRFLRNTKKFISLGKHAKLSLQELTWKMSVRDCAWLRRSPGVGCVPAAEHRLREEI 814

Qy        541 LAKFLHWLMSVYVVELLRSFFYVTETTFQKNRLFFYRKSVWSKLQSIGIRQHLKRVQLRE 600
              |||||||||||||||||||||||||||||||||||| ||||||||||||||||||||||
Db        815 LAKFLHWLMSVYVVELLRSFFYVTETTFQKNRLFFYRPSVWSKLQSIGIRQHLKRVQLRE 874

Qy        601 LSEAEVRQHREARPALLTSRLRFIPKPDGLRPIVNMDYVVGARTFRREKRAERLTSRVKA 660
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        875 LSEAEVRQHREARPALLTSRLRFIPKPDGLRPIVNMDYVVGARTFRREKRAERLTSRVKA 934

Qy        661 LFSVLNYERARRPGLLGASVLGLDDIHRAWRTFVLRVRAQDPPPELYFVKVDVTGAYDTI 720
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        935 LFSVLNYERARRPGLLGASVLGLDDIHRAWRTFVLRVRAQDPPPELYFVKVDVTGAYDTI 994

Qy        721 PQDRLTEVIASIIKPQNTYCVRRYAVVQKAAHGHVRKAFKSHVSTLTDLQPYMRQFVAHL 780
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        995 PQDRLTEVIASIIKPQNTYCVRRYAVVQKAAHGHVRKAFKSHVSTLTDLQPYMRQFVAHL 1054

Qy        781 QETSPLRDAVVIEQSSSLNEASSGLFDVFLRFMCHHAVRIRGKSYVQCQGIPQGSILSTL 840
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1055 QETSPLRDAVVIEQSSSLNEASSGLFDVFLRFMCHHAVRIRGKSYVQCQGIPQGSILSTL 1114

Qy        841 LCSLCYGDMENKLFAGIRRDGLLLRLVDDFLLVTPHLTHAKTFLRTLVRGVPEYGCVVNL 900
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1115 LCSLCYGDMENKLFAGIRRDGLLLRLVDDFLLVTPHLTHAKTFLRTLVRGVPEYGCVVNL 1174

Qy        901 RKTVVNFPVEDEALGGTAFVQMPAHGLFPWCGLLLDTRTLEVQSDYSSYARTSIRASLTF 960
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||:||
Db       1175 RKTVVNFPVEDEALGGTAFVQMPAHGLFPWCGLLLDTRTLEVQSDYSSYARTSIRASVTF 1234

Qy        961 NRGFKAGRNMRRKLFGVLRLKCHSLFLDLQVNSLQTVCTNIYKILLLQAYRFHACVLQLP 1020
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1235 NRGFKAGRNMRRKLFGVLRLKCHSLFLDLQVNSLQTVCTNIYKILLLQAYRFHACVLQLP 1294

Qy       1021 FHQQVWKNPTFFLRVISDTASLCYSILKAKNAGMSLGAKGAAGPLPSEAVQWLCHQAFLL 1080
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1295 FHQQVWKNPTFFLRVISDTASLCYSILKAKNAGMSLGAKGAAGPLPSEAVQWLCHQAFLL 1354

Qy       1081 KLTRHRVTYVPLLGSLRTAQTQLSRKLPGTTLTALEAAANPALPSDFKTILD 1132
              ||||||||||||||| ||||||||||||||||||||||||||||||||||
Db       1355 KLTRHRVTYVPLLGSL-TAQTQLSRKLPGTTLTALEAAANPALPSDFKTILD 1405
```

RESULT 35
AAW47007
ID AAW47007 standard; protein; 1199 AA.
XX
AC AAW47007;
XX
DT 13-AUG-1998 (first entry)
XX
DE Glutathione-S-transferase and hTRT fusion protein 7.
XX
KW Human; telomerase reverse transcriptase; hTRT; TRT; diagnosis; prognosis;
KW cell proliferation; cancer; ageing; ribonucleoprotein.
XX

```
OS   Synthetic.
OS   Homo sapiens.
XX
FH   Key             Location/Qualifiers
FT   Misc-difference 32. .33
FT                   /note= "enterokinase cleavage site"
XX
PN   GB2317891-A.
XX
PD   08-APR-1998.
XX
PF   01-OCT-1997;    97GB-00020890.
XX
PR   01-OCT-1996;    96US-00724643.
PR   18-APR-1997;    97US-00844419.
PR   25-APR-1997;    97US-00846017.
PR   06-MAY-1997;    97US-00851843.
PR   09-MAY-1997;    97US-00854050.
PR   14-AUG-1997;    97US-00911312.
PR   14-AUG-1997;    97US-00912951.
PR   14-AUG-1997;    97US-00915503.
XX
PA   (GERO-) GERON CORP.
PA   (UYTE-) UNIV TECHNOLOGY CORP.
XX
PI   Cech TR,  Lingner J,  Nakamura T,  Chapman KB,  Morin GB,  Harley CB;
PI   Andrews WH;
XX
DR   WPI; 1998-171633/16.
XX
PT   Pure and recombinant human Telomerase Reverse Transcriptase and its
PT   variants - are useful in the diagnosis, prognosis and treatment of cell
PT   proliferation conditions especially cancer and ageing.
XX
PS   Example 6; Page 233; 387pp; English.
XX
CC   The present sequence represents a fusion protein from an example of the
CC   present invention which describes human telomerase reverse transcriptase
CC   (hTRT). The present invention also describes the following methods: (A)
CC   determining whether a test compound is a modulator of hTRT, by detecting
CC   the change in hTRT recombinant protein or polynucleotide, on
CC   administration of the compound; (B) preparation of recombinant telomerase
CC   by contacting a protein preparation of hTRT with a telomerase RNA
CC   component; (C) detection of the hTRT RNA or protein in a sample by
CC   binding a relevant probe to the sample and detecting the complex formed
CC   or in the case of RNA detection, amplifying the product and correlating
CC   the presence of complex or amplification product with presence of hTRT in
CC   the sample; and (D) increasing the proliferation of a vertebrate cell by
CC   increasing hTRT expression; and (E) the use of an agent that causes an
CC   increase in cell vertebrate cell proliferation to create a medicament
CC   that inhibits ageing. A protein preparation of hTRT and the
CC   polynucleotide encoding hTRT can be used in the manufacture of
CC   medicaments for inhibiting the effect of ageing or cancer. Inhibitors of
CC   telomerase activity can be used to treat conditions that are associated
CC   with high telomerase activity. A protein preparation of hTRT can also be
CC   used in the new methods
XX
SQ   Sequence 1199 AA;

  Query Match             99.2%;  Score 5911.5;  DB 2;  Length 1199;
  Best Local Similarity   99.6%;  Pred. No. 0;
  Matches 1129;  Conservative    0;  Mismatches    1;  Indels    3;  Gaps    3;

Qy          1 MPRAPRCRAVRSLLRSHYREVLPLATFVRRLGPQGWRLVQRGDPAAFRALVAQCLVCVPW 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         69 MPRAPRCRAVRSLLRSHYREVLPLATFVRRLGPQGWRLVQRGDPAAFRALVAQCLVCVPW 128

Qy         61 DARPPPAAPSFRQVSCLK-ELVARVLQRLCERGAKNVLAFGFALLDGARGGPPEAFTTSV 119
              |||||||||||||||| ||||||||||||||||||||||||||||||||||||||||||
Db        129 DARPPPAAPSFRQVSCLKLELVARVLQRLCERGAKNVLAFGFALLDGARGGPPEAFTTSV 188

Qy        120 RSYLPNTVTDALRGSGAWGLLLRRVGDDVLVHLLARCALFVLVAPSCAYQVCGPPLYQLG 179
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||

Db        189 RSYLPNTVTDALRGSGAWGLLLRRVGDDVLVHLLARCALFVLVAPSCAYQVCGPPLYQLG 248

Qy        180 AATQARPPPHASGPRRRLGCERAWNHSVREAGVPLGLPAPGARRRGGSASRSLPLPKRPR 239
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        249 AATQARPPPHASGPRRRLGCERAWNHSVREAGVPLGLPAPGARRRGGSASRSLPLPKRPR 308

Qy        240 RGAAPEPERTPVGQGSWAHPGRTRGPSDRGFCVVSPARPAEEATSLEGALSGTRHSHPSV 299
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        309 RGAAPEPERTPVGQGSWAHPGRTRGPSDRGFCVVSPARPAEEATSLEGALSGTRHSHPSV 368

Qy        300 GRQHHAGPPSTSRPPRPWDTPCPPVYAETKHFLYSSGDKEQLRPSFLLSSLRPSLTGARR 359
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        369 GRQHHAGPPSTSRPPRPWDTPCPPVYAETKHFLYSSGDKEQLRPSFLLSSLRPSLTGARR 428

Qy        360 LVETIFLGSRPWMPGTPRRLPRLPQRYWQMRPLFLELLGNHAQCPYGVLLKTHCPLRAAV 419
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        429 LVETIFLGSRPWMPGTPRRLPRLPQRYWQMRPLFLELLGNHAQCPYGVLLKTHCPLRAAV 488

Qy        420 TPAAGVCAREKPQGSVAAPEEEDTDPRRLVQLLRQHSSPWQVYGFVRACLRRLVPPGLWG 479
              |||||||||| ||||||||||||||||||||||||||||||||||||||||||||||||
Db        489 TPAAGVCAREM-QGSVAAPEEEDTDPRRLVQLLRQHSSPWQVYGFVRACLRRLVPPGLWG 547

Qy        480 SRHNERRFLRNTKKFISLGKHAKLSLQELTWKMSVRDCAWLRRSPGVGCVPAAEHRLREE 539
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        548 SRHNERRFLRNTKKFISLGKHAKLSLQELTWKMSVRDCAWLRRSPGVGCVPAAEHRLREE 607

Qy        540 ILAKFLHWLMSVYVVELLRSFFYVTETTFQKNRLFFYRKSVWSKLQSIGIRQHLKRVQLR 599
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        608 ILAKFLHWLMSVYVVELLRSFFYVTETTFQKNRLFFYRKSVWSKLQSIGIRQHLKRVQLR 667

Qy        600 ELSEAEVRQHREARPALLTSRLRFIPKPDGLRPIVNMDYVVGARTFRREKRAERLTSRVK 659
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        668 ELSEAEVRQHREARPALLTSRLRFIPKPDGLRPIVNMDYVVGARTFRREKRAERLTSRVK 727

Qy        660 ALFSVLNYERARRPGLLGASVLGLDDIHRAWRTFVLRVRAQDPPPELYFVKVDVTGAYDT 719
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        728 ALFSVLNYERARRPGLLGASVLGLDDIHRAWRTFVLRVRAQDPPPELYFVKVDVTGAYDT 787

Qy        720 IPQDRLTEVIASIIKPQNTYCVRRYAVVQKAAHGHVRKAFKSHVSTLTDLQPYMRQFVAH 779
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        788 IPQDRLTEVIASIIKPQNTYCVRRYAVVQKAAHGHVRKAFKSHVSTLTDLQPYMRQFVAH 847

Qy        780 LQETSPLRDAVVIEQSSSLNEASSGLFDVFLRFMCHHAVRIRGKSYVQCQGIPQGSILST 839
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        848 LQETSPLRDAVVIEQSSSLNEASSGLFDVFLRFMCHHAVRIRGKSYVQCQGIPQGSILST 907

Qy        840 LLCSLCYGDMENKLFAGIRRDGLLLRLVDDFLLVTPHLTHAKTFLRTLVRGVPEYGCVVN 899
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        908 LLCSLCYGDMENKLFAGIRRDGLLLRLVDDFLLVTPHLTHAKTFLRTLVRGVPEYGCVVN 967

Qy        900 LRKTVVNFPVEDEALGGTAFVQMPAHGLFPWCGLLLDTRTLEVQSDYSSYARTSIRASLT 959
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        968 LRKTVVNFPVEDEALGGTAFVQMPAHGLFPWCGLLLDTRTLEVQSDYSSYARTSIRASLT 1027

Qy        960 FNRGFKAGRNMRRKLFGVLRLKCHSLFLDLQVNSLQTVCTNIYKILLLQAYRFHACVLQL 1019
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1028 FNRGFKAGRNMRRKLFGVLRLKCHSLFLDLQVNSLQTVCTNIYKILLLQAYRFHACVLQL 1087

Qy       1020 PFHQQVWKNPTFFLRVISDTASLCYSILKAKNAGMSLGAKGAAGPLPSEAVQWLCHQAFL 1079
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1088 PFHQQVWKNPTFFLRVISDTASLCYSILKAKNAGMSLGAKGAAGPLPSEAVQWLCHQAFL 1147

Qy       1080 LKLTRHRVTYVPLLGSLRTAQTQLSRKLPGTTLTALEAAANPALPSDFKTILD 1132
              ||||||||||||||||||||||||||||| ||||||||||||||||||||||
Db       1148 LKLTRHRVTYVPLLGSLRTAQTQLSRKLPG-TLTALEAAANPALPSDFKTILD 1199


RESULT 36
AAY00641
ID   AAY00641 standard; protein; 1120 AA.
XX
AC   AAY00641;
XX
```

DT 26-JUL-1999 (first entry)
XX
DE Telomerase protein sequence lacking motif A.
XX
KW Telomerase; human; cancer; diagnosis; melanoma; skin cancer; leukaemia;
KW neuroblastoma; breast carcinoma; colon carcinoma; lymphoma; osteosarcoma;
KW smooth muscle cell hyperplasia; stem cell proliferation; Wilm's tumour;
KW stem cell differentiation; organ regeneration; organ differentiation.
XX
OS Homo sapiens.
OS Synthetic.
XX
PN WO9901560-A1.
XX
PD 14-JAN-1999.
XX
PF 01-JUL-1998; 98WO-US013835.
XX
PR 01-JUL-1997; 97US-0051410P.
PR 21-JUL-1997; 97US-0053018P.
PR 21-JUL-1997; 97US-0053329P.
PR 04-AUG-1997; 97US-0054642P.
PR 09-SEP-1997; 97US-0058287P.
XX
PA (CAMB-) CAMBIA BIOSYSTEMS LLC.
XX
PI Kilian A, Bowtell D;
XX
DR WPI; 1999-106060/09.
DR N-PSDB; AAX18269.
XX
PT New isolated vertebrate telomerase genes - used to develop products for
PT treating cancers or for organ regeneration, nerve cell or brain cell
PT growth following injury or bone marrow transplantation.
XX
PS Claim 4; Fig 11n-o; 134pp; English.
XX
CC This sequence is a truncated human telomerase of the invention. Primers
CC that amplify the telomerase coding sequence can be used in a method for
CC diagnosing cancer in a patient. The telomerase can be used for detection,
CC diagnosis and drug screening. Inhibitors of telomerase activity can be
CC used to treat cancers such as melanomas, other skin cancers,
CC neuroblastomas, breast carcinomas, colon carcinomas, leukaemias,
CC lymphomas, osteosarcomas or smooth muscle cell hyperplasias or skin
CC growths. Enhancers of telomerase may be used to stimulate stem cell
CC proliferation and differentiation (expansion of haematopoietic stem cells
CC could be administered in the bone marrow transplant context). As well,
CC many tissues have stem cells. Proliferation of these cells may be useful
CC in wound healing, hair growth, treatment of disease such as Wilm's
CC tumour, organ regeneration or differentiation after injury or diseases,
CC nerve cell or brain cell growth following injury
XX
SQ Sequence 1120 AA;

Query Match 98.7%; Score 5882; DB 2; Length 1120;
Best Local Similarity 98.9%; Pred. No. 0;
Matches 1120; Conservative 0; Mismatches 0; Indels 12; Gaps 1;

```
Qy          1 MPRAPRCRAVRSLLRSHYREVLPLATFVRRLGPQGWRLVQRGDPAAFRALVAQCLVCVPW 60
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 MPRAPRCRAVRSLLRSHYREVLPLATFVRRLGPQGWRLVQRGDPAAFRALVAQCLVCVPW 60

Qy         61 DARPPPAAPSFRQVSCLKELVARVLQRLCERGAKNVLAFGFALLDGARGGPPEAFTTSVR 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 DARPPPAAPSFRQVSCLKELVARVLQRLCERGAKNVLAFGFALLDGARGGPPEAFTTSVR 120

Qy        121 SYLPNTVTDALRGSGAWGLLLRRVGDDVLVHLLARCALFVLVAPSCAYQVCGPPLYQLGA 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 SYLPNTVTDALRGSGAWGLLLRRVGDDVLVHLLARCALFVLVAPSCAYQVCGPPLYQLGA 180

Qy        181 ATQARPPPHASGPRRRLGCERAWNHSVREAGVPLGLPAPGARRRGGSASRSLPLPKRPRR 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 ATQARPPPHASGPRRRLGCERAWNHSVREAGVPLGLPAPGARRRGGSASRSLPLPKRPRR 240

Qy        241 GAAPEPERTPVGQGSWAHPGRTRGPSDRGFCVVSPARPAEEATSLEGALSGTRHSHPSVG 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 GAAPEPERTPVGQGSWAHPGRTRGPSDRGFCVVSPARPAEEATSLEGALSGTRHSHPSVG 300

Qy        301 RQHHAGPPSTSRPPRPWDTPCPPVYAETKHFLYSSGDKEQLRPSFLLSSLRPSLTGARRL 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 RQHHAGPPSTSRPPRPWDTPCPPVYAETKHFLYSSGDKEQLRPSFLLSSLRPSLTGARRL 360

Qy        361 VETIFLGSRPWMPGTPRRLPRLPQRYWQMRPLFLELLGNHAQCPYGVLLKTHCPLRAAVT 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        361 VETIFLGSRPWMPGTPRRLPRLPQRYWQMRPLFLELLGNHAQCPYGVLLKTHCPLRAAVT 420

Qy        421 PAAGVCAREKPQGSVAAPEEEDTDPRRLVQLLRQHSSPWQVYGFVRACLRRLVPPGLWGS 480
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        421 PAAGVCAREKPQGSVAAPEEEDTDPRRLVQLLRQHSSPWQVYGFVRACLRRLVPPGLWGS 480

Qy        481 RHNERRFLRNTKKFISLGKHAKLSLQELTWKMSVRDCAWLRRSPGVGCVPAAEHRLREEI 540
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        481 RHNERRFLRNTKKFISLGKHAKLSLQELTWKMSVRDCAWLRRSPGVGCVPAAEHRLREEI 540

Qy        541 LAKFLHWLMSVYVVELLRSFFYVTETTFQKNRLFFYRKSVWSKLQSIGIRQHLKRVQLRE 600
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        541 LAKFLHWLMSVYVVELLRSFFYVTETTFQKNRLFFYRKSVWSKLQSIGIRQHLKRVQLRE 600

Qy        601 LSEAEVRQHREARPALLTSRLRFIPKPDGLRPIVNMDYVVGARTFRREKRAERLTSRVKA 660
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        601 LSEAEVRQHREARPALLTSRLRFIPKPDGLRPIVNMDYVVGARTFRREKRAERLTSRVKA 660

Qy        661 LFSVLNYERARRPGLLGASVLGLDDIHRAWRTFVLRVRAQDPPPELYFVKVDVTGAYDTI 720
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        661 LFSVLNYERARRPGLLGASVLGLDDIHRAWRTFVLRVRAQDPPPELYFVK---------- 710

Qy        721 PQDRLTEVIASIIKPQNTYCVRRYAVVQKAAHGHVRKAFKSHVSTLTDLQPYMRQFVAHL 780
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        711 --DRLTEVIASIIKPQNTYCVRRYAVVQKAAHGHVRKAFKSHVSTLTDLQPYMRQFVAHL 768

Qy        781 QETSPLRDAVVIEQSSSLNEASSGLFDVFLRFMCHHAVRIRGKSYVQCQGIPQGSILSTL 840
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        769 QETSPLRDAVVIEQSSSLNEASSGLFDVFLRFMCHHAVRIRGKSYVQCQGIPQGSILSTL 828

Qy        841 LCSLCYGDMENKLFAGIRRDGLLLRLVDDFLLVTPHLTHAKTFLRTLVRGVPEYGCVVNL 900
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        829 LCSLCYGDMENKLFAGIRRDGLLLRLVDDFLLVTPHLTHAKTFLRTLVRGVPEYGCVVNL 888

Qy        901 RKTVVNFPVEDEALGGTAFVQMPAHGLFPWCGLLLDTRTLEVQSDYSSYARTSIRASLTF 960
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        889 RKTVVNFPVEDEALGGTAFVQMPAHGLFPWCGLLLDTRTLEVQSDYSSYARTSIRASLTF 948

Qy        961 NRGFKAGRNMRRKLFGVLRLKCHSLFLDLQVNSLQTVCTNIYKILLLQAYRFHACVLQLP 1020
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        949 NRGFKAGRNMRRKLFGVLRLKCHSLFLDLQVNSLQTVCTNIYKILLLQAYRFHACVLQLP 1008

Qy       1021 FHQQVWKNPTFFLRVISDTASLCYSILKAKNAGMSLGAKGAAGPLPSEAVQWLCHQAFLL 1080
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1009 FHQQVWKNPTFFLRVISDTASLCYSILKAKNAGMSLGAKGAAGPLPSEAVQWLCHQAFLL 1068

Qy       1081 KLTRHRVTYVPLLGSLRTAQTQLSRKLPGTTLTALEAAANPALPSDFKTILD 1132
              |||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1069 KLTRHRVTYVPLLGSLRTAQTQLSRKLPGTTLTALEAAANPALPSDFKTILD 1120
```

RESULT 37
AAY00650
ID AAY00650 standard; protein; 1120 AA.
XX
AC AAY00650;
XX
DT 26-JUL-1999 (first entry)
XX
DE Telomerase (ver. 2) protein sequence lacking motif A.
XX
KW Telomerase; human; cancer; diagnosis; melanoma; skin cancer; leukaemia;

```
KW   neuroblastoma; breast carcinoma; colon carcinoma; lymphoma; osteosarcoma;
KW   smooth muscle cell hyperplasia; stem cell proliferation; Wilm's tumour;
KW   stem cell differentiation; organ regeneration; organ differentiation.
XX
OS   Homo sapiens.
OS   Synthetic.
XX
PN   WO9901560-A1.
XX
PD   14-JAN-1999.
XX
PF   01-JUL-1998;   98WO-US013835.
XX
PR   01-JUL-1997;   97US-0051410P.
PR   21-JUL-1997;   97US-0053018P.
PR   21-JUL-1997;   97US-0053329P.
PR   04-AUG-1997;   97US-0054642P.
PR   09-SEP-1997;   97US-0058287P.
XX
PA   (CAMB-) CAMBIA BIOSYSTEMS LLC.
XX
PI   Kilian A,  Bowtell D;
XX
DR   WPI; 1999-106060/09.
DR   N-PSDB; AAX18278.
XX
PT   New isolated vertebrate telomerase genes - used to develop products for
PT   treating cancers or for organ regeneration, nerve cell or brain cell
PT   growth following injury or bone marrow transplantation.
XX
PS   Claim 4; Fig 11ah-aj; 134pp; English.
XX
CC   This sequence is a truncated human telomerase of the invention. Primers
CC   that amplify the telomerase coding sequence can be used in a method for
CC   diagnosing cancer in a patient. The telomerase can be used for detection,
CC   diagnosis and drug screening. Inhibitors of telomerase activity can be
CC   used to treat cancers such as melanomas, other skin cancers,
CC   neuroblastomas, breast carcinomas, colon carcinomas, leukaemias,
CC   lymphomas, osteosarcomas or smooth muscle cell hyperplasias or skin
CC   growths. Enhancers of telomerase may be used to stimulate stem cell
CC   proliferation and differentiation (expansion of haematopoietic stem cells
CC   could be administered in the bone marrow transplant context). As well,
CC   many tissues have stem cells. Proliferation of these cells may be useful
CC   in wound healing, hair growth, treatment of disease such as Wilm's
CC   tumour, organ regeneration or differentiation after injury or diseases,
CC   nerve cell or brain cell growth following injury. Note: The N-terminus of
CC   this sequence can be replaced by the sequences shown in AAY00656-Y00658
XX
SQ   Sequence 1120 AA;

  Query Match             98.5%;  Score 5873;  DB 2;  Length 1120;
  Best Local Similarity   98.9%;  Pred. No. 0;
  Matches 1119;  Conservative    0;  Mismatches    1;  Indels   12;  Gaps    1;

Qy          1 MPRAPRCRAVRSLLRSHYREVLPLATFVRRLGPQGWRLVQRGDPAAFRALVAQCLVCVPW 60
              ||||||||||||||| |||||||||||||||||||||||||||||||||||||||||||
Db          1 MPRAPRCRAVRSLLRSHTREVLPLATFVRRLGPQGWRLVQRGDPAAFRALVAQCLVCVPW 60

Qy         61 DARPPPAAPSFRQVSCLKELVARVLQRLCERGAKNVLAFGFALLDGARGGPPEAFTTSVR 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 DARPPPAAPSFRQVSCLKELVARVLQRLCERGAKNVLAFGFALLDGARGGPPEAFTTSVR 120

Qy        121 SYLPNTVTDALRGSGAWGLLLRRVGDDVLVHLLARCALFVLVAPSCAYQVCGPPLYQLGA 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 SYLPNTVTDALRGSGAWGLLLRRVGDDVLVHLLARCALFVLVAPSCAYQVCGPPLYQLGA 180

Qy        181 ATQARPPPHASGPRRRLGCERAWNHSVREAGVPLGLPAPGARRRGGSASRSLPLPKRPRR 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 ATQARPPPHASGPRRRLGCERAWNHSVREAGVPLGLPAPGARRRGGSASRSLPLPKRPRR 240

Qy        241 GAAPEPERTPVGQGSWAHPGRTRGPSDRGFCVVSPARPAEEATSLEGALSGTRHSHPSVG 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 GAAPEPERTPVGQGSWAHPGRTRGPSDRGFCVVSPARPAEEATSLEGALSGTRHSHPSVG 300

Qy        301 RQHHAGPPSTSRPPRPWDTPCPPVYAETKHFLYSSGDKEQLRPSFLLSSLRPSLTGARRL 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 RQHHAGPPSTSRPPRPWDTPCPPVYAETKHFLYSSGDKEQLRPSFLLSSLRPSLTGARRL 360

Qy        361 VETIFLGSRPWMPGTPRRLPRLPQRYWQMRPLFLELLGNHAQCPYGVLLKTHCPLRAAVT 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        361 VETIFLGSRPWMPGTPRRLPRLPQRYWQMRPLFLELLGNHAQCPYGVLLKTHCPLRAAVT 420

Qy        421 PAAGVCAREKPQGSVAAPEEEDTDPRRLVQLLRQHSSPWQVYGFVRACLRRLVPPGLWGS 480
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        421 PAAGVCAREKPQGSVAAPEEEDTDPRRLVQLLRQHSSPWQVYGFVRACLRRLVPPGLWGS 480

Qy        481 RHNERRFLRNTKKFISLGKHAKLSLQELTWKMSVRDCAWLRRSPGVGCVPAAEHRLREEI 540
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        481 RHNERRFLRNTKKFISLGKHAKLSLQELTWKMSVRDCAWLRRSPGVGCVPAAEHRLREEI 540

Qy        541 LAKFLHWLMSVYVVELLRSFFYVTETTFQKNRLFFYRKSVWSKLQSIGIRQHLKRVQLRE 600
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        541 LAKFLHWLMSVYVVELLRSFFYVTETTFQKNRLFFYRKSVWSKLQSIGIRQHLKRVQLRE 600

Qy        601 LSEAEVRQHREARPALLTSRLRFIPKPDGLRPIVNMDYVVGARTFRREKRAERLTSRVKA 660
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        601 LSEAEVRQHREARPALLTSRLRFIPKPDGLRPIVNMDYVVGARTFRREKRAERLTSRVKA 660

Qy        661 LFSVLNYERARRPGLLGASVLGLDDIHRAWRTFVLRVRAQDPPPELYFVKVDVTGAYDTI 720
              ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        661 LFSVLNYERARRPGLLGASVLGLDDIHRAWRTFVLRVRAQDPPPELYFVK---------- 710

Qy        721 PQDRLTEVIASIIKPQNTYCVRRYAVVQKAAHGHVRKAFKSHVSTLTDLQPYMRQFVAHL 780
                  ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        711 --DRLTEVIASIIKPQNTYCVRRYAVVQKAAHGHVRKAFKSHVSTLTDLQPYMRQFVAHL 768

Qy        781 QETSPLRDAVVIEQSSSLNEASSGLFDVFLRFMCHHAVRIRGKSYVQCQGIPQGSILSTL 840
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        769 QETSPLRDAVVIEQSSSLNEASSGLFDVFLRFMCHHAVRIRGKSYVQCQGIPQGSILSTL 828

Qy        841 LCSLCYGDMENKLFAGIRRDGLLLRLVDDFLLVTPHLTHAKTFLRTLVRGVPEYGCVVNL 900
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        829 LCSLCYGDMENKLFAGIRRDGLLLRLVDDFLLVTPHLTHAKTFLRTLVRGVPEYGCVVNL 888

Qy        901 RKTVVNFPVEDEALGGTAFVQMPAHGLFPWCGLLLDTRTLEVQSDYSSYARTSIRASLTF 960
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        889 RKTVVNFPVEDEALGGTAFVQMPAHGLFPWCGLLLDTRTLEVQSDYSSYARTSIRASLTF 948

Qy        961 NRGFKAGRNMRRKLFGVLRLKCHSLFLDLQVNSLQTVCTNIYKILLLQAYRFHACVLQLP 1020
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        949 NRGFKAGRNMRRKLFGVLRLKCHSLFLDLQVNSLQTVCTNIYKILLLQAYRFHACVLQLP 1008

Qy       1021 FHQQVWKNPTFFLRVISDTASLCYSILKAKNAGMSLGAKGAAGPLPSEAVQWLCHQAFLL 1080
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1009 FHQQVWKNPTFFLRVISDTASLCYSILKAKNAGMSLGAKGAAGPLPSEAVQWLCHQAFLL 1068

Qy       1081 KLTRHRVTYVPLLGSLRTAQTQLSRKLPGTTLTALEAAANPALPSDFKTILD 1132
              ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1069 KLTRHRVTYVPLLGSLRTAQTQLSRKLPGTTLTALEAAANPALPSDFKTILD 1120


RESULT 38
AAW47006
ID   AAW47006 standard; protein; 1150 AA.
XX
AC   AAW47006;
XX
DT   13-AUG-1998  (first entry)
XX
DE   Glutathione-S-transferase and hTRT fusion protein 6.
XX
KW   Human; telomerase reverse transcriptase; hTRT; TRT; diagnosis; prognosis;
KW   cell proliferation; cancer; ageing; ribonucleoprotein.
XX
OS   Synthetic.
OS   Homo sapiens.
```

XX
PN GB2317891-A.
XX
PD 08-APR-1998.
XX
PF 01-OCT-1997; 97GB-00020890.
XX
PR 01-OCT-1996; 96US-00724643.
PR 18-APR-1997; 97US-00844419.
PR 25-APR-1997; 97US-00846017.
PR 06-MAY-1997; 97US-00851843.
PR 09-MAY-1997; 97US-00854050.
PR 14-AUG-1997; 97US-00911312.
PR 14-AUG-1997; 97US-00912951.
PR 14-AUG-1997; 97US-00915503.
XX
PA (GERO-) GERON CORP.
PA (UYTE-) UNIV TECHNOLOGY CORP.
XX
PI Cech TR, Lingner J, Nakamura T, Chapman KB, Morin GB, Harley CB;
PI Andrews WH;
XX
DR WPI; 1998-171633/16.
XX
PT Pure and recombinant human Telomerase Reverse Transcriptase and its
PT variants - are useful in the diagnosis, prognosis and treatment of cell
PT proliferation conditions especially cancer and ageing.
XX
PS Example 6; Page 231-232; 387pp; English.
XX
CC The present sequence represents a fusion protein from an example of the
CC present invention which describes human telomerase reverse transcriptase
CC (hTRT). The present invention also describes the following methods: (A)
CC determining whether a test compound is a modulator of hTRT, by detecting
CC the change in hTRT recombinant protein or polynucleotide, on
CC administration of the compound; (B) preparation of recombinant telomerase
CC by contacting a protein preparation of hTRT with a telomerase RNA
CC component; (C) detection of the hTRT RNA or protein in a sample by
CC binding a relevant probe to the sample and detecting the complex formed
CC or in the case of RNA detection, amplifying the product and correlating
CC the presence of complex or amplification product with presence of hTRT in
CC the sample; and (D) increasing the proliferation of a vertebrate cell by
CC increasing hTRT expression; and (E) the use of an agent that causes an
CC increase in cell vertebrate cell proliferation to create a medicament
CC that inhibits ageing. A protein preparation of hTRT and the
CC polynucleotide encoding hTRT can be used in the manufacture of
CC medicaments for inhibiting the effect of ageing or cancer. Inhibitors of
CC telomerase activity can be used to treat conditions that are associated
CC with high telomerase activity. A protein preparation of hTRT can also be
CC used in the new methods
XX
SQ Sequence 1150 AA;

Query Match 96.0%; Score 5721; DB 2; Length 1150;
Best Local Similarity 97.8%; Pred. No. 0;
Matches 1112; Conservative 6; Mismatches 5; Indels 14; Gaps 13;

```
Qy          1 MPRAPRCRAVRSLLRSHYREVLPLATFVRRLGPQGWRLVQRGDPAAFRALVAQCLVCVPW 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 MPRAPRCRAVRSLLRSHYREVLPLATFVRRLGPQGWRLVQRGDPAAFRALVAQCLVCVPW 60

Qy         61 DARPPPAAPSFRQVSCLKELVARVLQRLCERGAKNVLAFGFALLDGARGGPPEAFTTSVR 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 DARPPPAAPSFRQVSCLKELVARVLQRLCERGAKNVLAFGFALLDGARGGPPEAFTTSVR 120

Qy        121 SYLPNTVTDALRGSGAWGLLLRRVGDDVLVHLLARCALFVLVAPSCAYQVCGPPLYQLGA 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 SYLPNTVTDALRGSGAWGLLLRRVGDDVLVHLLARCALFVLVAPSCAYQVCGPPLYQLGA 180

Qy        181 ATQARPPPHASGPRRRLGCERAWNHSVREAGVPLGLPAPGARRRGGSASRSLPLPKRPRR 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 ATQARPPPHASGPRRRLGCERAWNHSVREAGVPLGLPAPGARRRGGSASRSLPLPKRPRR 240

Qy        241 GAAPEPERTPVGQGSWAHPGRTRGPSDRGFCVVSPARPAEEATSLEGALSGTRHSHPSVG 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 GAAPEPERTPVGQGSWAHPGRTRGPSDRGFCVVSPARPAEEATSLEGALSGTRHSHPSVG 300

Qy        301 RQHHAGPPSTSRPPRPWDTPCPPVYAETKHFLYSSGDKEQLRPSFLLSSLRPSLTGARRL 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 RQHHAGPPSTSRPPRPWDTPCPPVYAETKHFLYSSGDKEQLRPSFLLSSLRPSLTGARRL 360

Qy        361 VETIFLGSRPWMPGTPRRLPRLPQRYWQMRPLFLELLGNHAQCPYGVLLKTHCPLRAAVT 420
              |||||||| ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        361 VETIFLGS-PWMPGTPRRLPRLPQRYWQMRPLFLELLGNHAQCPYGVLLKTHCPLRAAVT 419

Qy        421 PAAGVCAREKPQGSVAAPEEEDTDPRRLVQLLRQHSSPWQVYGFVRACLRRLVPPGL-WG 479
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||  |
Db        420 PAAGVCAREKPQGSVAAPEEEDTDPRRLVQLLRQHSSPWQVYGFVRACLRRLVPPGLEVG 479

Qy        480 SRHNERRFLRNTKKFISLGKHAKLSLQELTWKMSVRDCAWLRRSPGVGCVPAAEHRLREE 539
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        480 SRHNERRFLRNTKKFISLGKHAKLSLQELTWKMSVRDCAWLRRSPGVGCVPAAEHRLREE 539

Qy        540 ILAKFLHWLMSVYVVELLRSFFYVTETTFQKNRLFFYRKSVWSKLQSIGIRQHLKRVQLR 599
              |||||||||||||||||||||||: ||||||||||||||||||||||||||||||||||||
Db        540 ILAKFLHWLMSVYVVELLRSFFW-TETTFQKNRLFFYRKSVWSKLQSIGIRQHLKRVQLR 598

Qy        600 ELSEAEVRQHREARPALLTSRLRFIPKPDGLRPIVN-MDYVVGARTFRREKRAERLTSRV 658
              |||||||||||||||||||||||||||||||||||| ||: ||||||||||||||||||||
Db        599 ELSEAEVRQHREARPALLTSRLRFIPKPDGLRPIVNTMDW-VGARTFRREKRAERLTSRV 657

Qy        659 KALFSVLNYERARRPGLLGASVLGLDDIHRAWRTFVLRVRAQDPPPELYFVKVDVTGAYD 718
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        658 KALFSVLNYERARRPGLLGASVLGLDDIHRAWRTFVLRVRAQDPPPELYFVKVDVTGAYD 717

Qy        719 TIPQDRLTEVIASIIKPQNTYCVRRYAVVQKAAHGHVRKAFKSHVSTLTDLQPYMRQFVA 778
              |||||||||||||:||||||||||||||||||||||||||||||||||||||||||||||
Db        718 TIPQDRLTEVIASLIKPQNTYCVRRYAVVQKAAHGHVRKAFKSHVSTLTDLQPYMRQFVA 777

Qy        779 HLQETSPLRDAVVIEQSSSL-NEASSGLFDVFLRFMCHHAVRIRGKSYVQCQGIPQGSIL 837
              |||||||||||||||||||  ||||||||||||||||||  ||||: ||||||||||:
Db        778 HLQETSPLRDAVVIEQSSSLETEASSGLFDVFLRFMCHHAVE-RGKSW-QCQGIPQGSII 835

Qy        838 STLLCSLCYGDMENKLFAGIRRDGLLLRLVDDFLLVTPHLTHAKTFLRTLVRGVPEYGCV 897
              |||||||||||||||||||||||||||||||||||||||||||||||:|||||| ||||||
Db        836 STLLCSLCYGDMENKLFAGIRRDGLLLRLVDDFLLVTPHLTHAKTFIRTLVRG-PEYGCV 894

Qy        898 VNLRKTVVNFPVEDEALGGTAFVQMPAHGLFPW-CGLLLDTRTLEVQSDYSSYARTSIRA 956
              |||||||  |||||||||||||||||||||||| |||||||||||||| ||||||||||
Db        895 VNLRKTV--FPVEDEALGGTAFVQMPAHGLFPWVCGLLLDTRTLEVQSDESSYARTSIRA 952

Qy        957 SLTFNRGFKAGR-NMRRKLFGVLRLKCHSLFLDLQVNSLQTVCTNIYKILLLQAYRFHAC 1015
              |||||||||||  ||||||||||||||||||||||||||||||||||||||||||||||
Db        953 SLTFNRGFKAGRETMRRKLFGVLRLKCHSLFLDLQVNSLQTVCTNIYKILLLQAYRFHAC 1012

Qy       1016 VLQLPFHQQVWKNPTFFLRVISDTASLCYSILKAKNAGMSLGAKGAAGPLPSEAVQWLCH 1075
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1013 VLQLPFHQQVWKNPTFFLRVISDTASLCYSILKAKNAGMSLGAKGAAGPLPSEAVQWLCH 1072

Qy       1076 QAFLLKLTRHRVTYVPLLGSLRTAQTQLSRKLPGTTLTALEAAANPALPSDFKTILD 1132
              |||||||||||||||||||||||||||||||||||||||||||||| ||||||||
Db       1073 QAFLLKLTRHRVTYVPLLGSLRTAQTQLSRKLPGTTLTALEAAANPAL-SDFKTILD 1128
```

RESULT 39
AAY00640
ID AAY00640 standard; protein; 1053 AA.
XX
AC AAY00640;
XX
DT 26-JUL-1999 (first entry)
XX
DE Altered C-terminused telomerase protein sequence.
XX
KW Telomerase; human; cancer; diagnosis; melanoma; skin cancer; leukaemia;
KW neuroblastoma; breast carcinoma; colon carcinoma; lymphoma; osteosarcoma;

```
KW   smooth muscle cell hyperplasia; stem cell proliferation; Wilm's tumour;
KW   stem cell differentiation; organ regeneration; organ differentiation.
XX
OS   Homo sapiens.
OS   Synthetic.
XX
PN   WO9901560-A1.
XX
PD   14-JAN-1999.
XX
PF   01-JUL-1998;   98WO-US013835.
XX
PR   01-JUL-1997;   97US-0051410P.
PR   21-JUL-1997;   97US-0053018P.
PR   21-JUL-1997;   97US-0053329P.
PR   04-AUG-1997;   97US-0054642P.
PR   09-SEP-1997;   97US-0058287P.
XX
PA   (CAMB-) CAMBIA BIOSYSTEMS LLC.
XX
PI   Kilian A,  Bowtell D;
XX
DR   WPI; 1999-106060/09.
DR   N-PSDB; AAX18268.
XX
PT   New isolated vertebrate telomerase genes - used to develop products for
PT   treating cancers or for organ regeneration, nerve cell or brain cell
PT   growth following injury or bone marrow transplantation.
XX
PS   Claim 4; Fig 11l-m; 134pp; English.
XX
CC   This sequence is a truncated human telomerase of the invention. Primers
CC   that amplify the telomerase coding sequence can be used in a method for
CC   diagnosing cancer in a patient. The telomerase can be used for detection,
CC   diagnosis and drug screening. Inhibitors of telomerase activity can be
CC   used to treat cancers such as melanomas, other skin cancers,
CC   neuroblastomas, breast carcinomas, colon carcinomas, leukaemias,
CC   lymphomas, osteosarcomas or smooth muscle cell hyperplasias or skin
CC   growths. Enhancers of telomerase may be used to stimulate stem cell
CC   proliferation and differentiation (expansion of haematopoietic stem cells
CC   could be administered in the bone marrow transplant context). As well,
CC   many tissues have stem cells. Proliferation of these cells may be useful
CC   in wound healing, hair growth, treatment of disease such as Wilm's
CC   tumour, organ regeneration or differentiation after injury or diseases,
CC   nerve cell or brain cell growth following injury. Note: The C-terminus of
CC   this sequence can be replaced by the sequence shown in AAY00654
XX
SQ   Sequence 1053 AA;

  Query Match             93.2%;  Score 5555;  DB 2;  Length 1053;
  Best Local Similarity   100.0%;  Pred. No. 0;
  Matches 1052;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 MPRAPRCRAVRSLLRSHYREVLPLATFVRRLGPQGWRLVQRGDPAAFRALVAQCLVCVPW 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 MPRAPRCRAVRSLLRSHYREVLPLATFVRRLGPQGWRLVQRGDPAAFRALVAQCLVCVPW 60

Qy         61 DARPPPAAPSFRQVSCLKELVARVLQRLCERGAKNVLAFGFALLDGARGGPPEAFTTSVR 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 DARPPPAAPSFRQVSCLKELVARVLQRLCERGAKNVLAFGFALLDGARGGPPEAFTTSVR 120

Qy        121 SYLPNTVTDALRGSGAWGLLLRRVGDDVLVHLLARCALFVLVAPSCAYQVCGPPLYQLGA 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 SYLPNTVTDALRGSGAWGLLLRRVGDDVLVHLLARCALFVLVAPSCAYQVCGPPLYQLGA 180

Qy        181 ATQARPPPHASGPRRRLGCERAWNHSVREAGVPLGLPAPGARRRGGSASRSLPLPKRPRR 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 ATQARPPPHASGPRRRLGCERAWNHSVREAGVPLGLPAPGARRRGGSASRSLPLPKRPRR 240

Qy        241 GAAPEPERTPVGQGSWAHPGRTRGPSDRGFCVVSPARPAEEATSLEGALSGTRHSHPSVG 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 GAAPEPERTPVGQGSWAHPGRTRGPSDRGFCVVSPARPAEEATSLEGALSGTRHSHPSVG 300

Qy        301 RQHHAGPPSTSRPPRPWDTPCPPVYAETKHFLYSSGDKEQLRPSFLLSSLRPSLTGARRL 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 RQHHAGPPSTSRPPRPWDTPCPPVYAETKHFLYSSGDKEQLRPSFLLSSLRPSLTGARRL 360

Qy        361 VETIFLGSRPWMPGTPRRLPRLPQRYWQMRPLFLELLGNHAQCPYGVLLKTHCPLRAAVT 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        361 VETIFLGSRPWMPGTPRRLPRLPQRYWQMRPLFLELLGNHAQCPYGVLLKTHCPLRAAVT 420

Qy        421 PAAGVCAREKPQGSVAAPEEEDTDPRRLVQLLRQHSSPWQVYGFVRACLRRLVPPGLWGS 480
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        421 PAAGVCAREKPQGSVAAPEEEDTDPRRLVQLLRQHSSPWQVYGFVRACLRRLVPPGLWGS 480

Qy        481 RHNERRFLRNTKKFISLGKHAKLSLQELTWKMSVRDCAWLRRSPGVGCVPAAEHRLREEI 540
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        481 RHNERRFLRNTKKFISLGKHAKLSLQELTWKMSVRDCAWLRRSPGVGCVPAAEHRLREEI 540

Qy        541 LAKFLHWLMSVYVVELLRSFFYVTETTFQKNRLFFYRKSVWSKLQSIGIRQHLKRVQLRE 600
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        541 LAKFLHWLMSVYVVELLRSFFYVTETTFQKNRLFFYRKSVWSKLQSIGIRQHLKRVQLRE 600

Qy        601 LSEAEVRQHREARPALLTSRLRFIPKPDGLRPIVNMDYVVGARTFRREKRAERLTSRVKA 660
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        601 LSEAEVRQHREARPALLTSRLRFIPKPDGLRPIVNMDYVVGARTFRREKRAERLTSRVKA 660

Qy        661 LFSVLNYERARRPGLLGASVLGLDDIHRAWRTFVLRVRAQDPPPELYFVKVDVTGAYDTI 720
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        661 LFSVLNYERARRPGLLGASVLGLDDIHRAWRTFVLRVRAQDPPPELYFVKVDVTGAYDTI 720

Qy        721 PQDRLTEVIASIIKPQNTYCVRRYAVVQKAAHGHVRKAFKSHVSTLTDLQPYMRQFVAHL 780
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        721 PQDRLTEVIASIIKPQNTYCVRRYAVVQKAAHGHVRKAFKSHVSTLTDLQPYMRQFVAHL 780

Qy        781 QETSPLRDAVVIEQSSSLNEASSGLFDVFLRFMCHHAVRIRGKSYVQCQGIPQGSILSTL 840
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        781 QETSPLRDAVVIEQSSSLNEASSGLFDVFLRFMCHHAVRIRGKSYVQCQGIPQGSILSTL 840

Qy        841 LCSLCYGDMENKLFAGIRRDGLLLRLVDDFLLVTPHLTHAKTFLRTLVRGVPEYGCVVNL 900
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        841 LCSLCYGDMENKLFAGIRRDGLLLRLVDDFLLVTPHLTHAKTFLRTLVRGVPEYGCVVNL 900

Qy        901 RKTVVNFPVEDEALGGTAFVQMPAHGLFPWCGLLLDTRTLEVQSDYSSYARTSIRASLTF 960
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        901 RKTVVNFPVEDEALGGTAFVQMPAHGLFPWCGLLLDTRTLEVQSDYSSYARTSIRASLTF 960

Qy        961 NRGFKAGRNMRRKLFGVLRLKCHSLFLDLQVNSLQTVCTNIYKILLLQAYRFHACVLQLP 1020
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        961 NRGFKAGRNMRRKLFGVLRLKCHSLFLDLQVNSLQTVCTNIYKILLLQAYRFHACVLQLP 1020

Qy       1021 FHQQVWKNPTFFLRVISDTASLCYSILKAKNA 1052
              ||||||||||||||||||||||||||||||||
Db       1021 FHQQVWKNPTFFLRVISDTASLCYSILKAKNA 1052


RESULT 40
AAY00649
ID   AAY00649 standard; protein; 1093 AA.
XX
AC   AAY00649;
XX
DT   26-JUL-1999  (first entry)
XX
DE   Altered C-terminus telomerase (ver. 2) protein sequence.
XX
KW   Telomerase; human; cancer; diagnosis; melanoma; skin cancer; leukaemia;
KW   neuroblastoma; breast carcinoma; colon carcinoma; lymphoma; osteosarcoma;
KW   smooth muscle cell hyperplasia; stem cell proliferation; Wilm's tumour;
KW   stem cell differentiation; organ regeneration; organ differentiation.
XX
OS   Homo sapiens.
OS   Synthetic.
XX
PN   WO9901560-A1.
XX
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PD   14-JAN-1999.
XX
PF   01-JUL-1998;   98WO-US013835.
XX
PR   01-JUL-1997;   97US-0051410P.
PR   21-JUL-1997;   97US-0053018P.
PR   21-JUL-1997;   97US-0053329P.
PR   04-AUG-1997;   97US-0054642P.
PR   09-SEP-1997;   97US-0058287P.
XX
PA   (CAMB-) CAMBIA BIOSYSTEMS LLC.
XX
PI   Kilian A,  Bowtell D;
XX
DR   WPI; 1999-106060/09.
DR   N-PSDB; AAX18277.
XX
PT   New isolated vertebrate telomerase genes - used to develop products for
PT   treating cancers or for organ regeneration, nerve cell or brain cell
PT   growth following injury or bone marrow transplantation.
XX
PS   Claim 4; Fig 11af-ag; 134pp; English.
XX
CC   This sequence is a truncated human telomerase of the invention. Primers
CC   that amplify the telomerase coding sequence can be used in a method for
CC   diagnosing cancer in a patient. The telomerase can be used for detection,
CC   diagnosis and drug screening. Inhibitors of telomerase activity can be
CC   used to treat cancers such as melanomas, other skin cancers,
CC   neuroblastomas, breast carcinomas, colon carcinomas, leukaemias,
CC   lymphomas, osteosarcomas or smooth muscle cell hyperplasias or skin
CC   growths. Enhancers of telomerase may be used to stimulate stem cell
CC   proliferation and differentiation (expansion of haematopoietic stem cells
CC   could be administered in the bone marrow transplant context). As well,
CC   many tissues have stem cells. Proliferation of these cells may be useful
CC   in wound healing, hair growth, treatment of disease such as Wilm's
CC   tumour, organ regeneration or differentiation after injury or diseases,
CC   nerve cell or brain cell growth following injury. Note: The N-terminus of
CC   this sequence can be replaced by the sequences shown in AAY00656-Y00658,
CC   and the C-terminus can be replaced by the sequence shown in AAY00654
XX
SQ   Sequence 1093 AA;

  Query Match             92.5%;  Score 5516;  DB 2;  Length 1093;
  Best Local Similarity   96.2%;  Pred. No. 0;
  Matches 1051;  Conservative    0;  Mismatches    1;  Indels   40;  Gaps    1;

Qy          1 MPRAPRCRAVRSLLRSHYREVLPLATFVRRLGPQGWRLVQRGDPAAFRALVAQCLVCVPW 60
              |||||||||||||||| ||||||||||||||||||||||||||||||||||||||||||
Db          1 MPRAPRCRAVRSLLRSHTREVLPLATFVRRLGPQGWRLVQRGDPAAFRALVAQCLVCVPW 60

Qy         61 DARPPPAAPSFRQVSCLKELVARVLQRLCERGAKNVLAFGFALLDGARGGPPEAFTTSVR 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 DARPPPAAPSFRQVSCLKELVARVLQRLCERGAKNVLAFGFALLDGARGGPPEAFTTSVR 120

Qy        121 SYLPNTVTDALRGSGAWGLLLRRVGDDVLVHLLARCALFVLVAPSCAYQVCGPPLYQLGA 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 SYLPNTVTDALRGSGAWGLLLRRVGDDVLVHLLARCALFVLVAPSCAYQVCGPPLYQLGA 180

Qy        181 ATQARPPPHASGPRRRLGCERAWNHSVREAGVPLGLPAPGARRRGGSASRSLPLPKRPRR 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 ATQARPPPHASGPRRRLGCERAWNHSVREAGVPLGLPAPGARRRGGSASRSLPLPKRPRR 240

Qy        241 GAAPEPERTPVGQGSWAHPGRTRGPSDRGFCVVSPARPAEEATSLEGALSGTRHSHPSVG 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 GAAPEPERTPVGQGSWAHPGRTRGPSDRGFCVVSPARPAEEATSLEGALSGTRHSHPSVG 300

Qy        301 RQHHAGPPSTSRPPRPWDTPCPPVYAETKHFLYSSGDKEQLRPSFLLSSLRPSLTGARRL 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 RQHHAGPPSTSRPPRPWDTPCPPVYAETKHFLYSSGDKEQLRPSFLLSSLRPSLTGARRL 360

Qy        361 VETIFLGSRPWMPGTPRRLPRLPQRYWQMRPLFLELLGNHAQCPYGVLLKTHCPLRAAVT 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        361 VETIFLGSRPWMPGTPRRLPRLPQRYWQMRPLFLELLGNHAQCPYGVLLKTHCPLRAAVT 420

Qy        421 PAAGVCAREKPQGSVAAPEEEDTDPRRLVQLLRQHSSPWQVYGFVRACLRRLVPPGLWGS 480
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        421 PAAGVCAREKPQGSVAAPEEEDTDPRRLVQLLRQHSSPWQVYGFVRACLRRLVPPGLWGS 480

Qy        481 RHNERRFLRNTKKFISLGKHAKLSLQE------------------------------ 507
              |||||||||||||||||||||||||||
Db        481 RHNERRFLRNTKKFISLGKHAKLSLQELTWKMSVRDCAWLRRSPGVGCVPAAEHRLREEI 540

Qy        508 -------LTWKMSVRDCAWLRRSPGVGCVPAAEHRLREEILAKFLHWLMSVYVVELLRSF 560
                    ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        541 LAKFLHWLTWKMSVRDCAWLRRSPGVGCVPAAEHRLREEILAKFLHWLMSVYVVELLRSF 600

Qy        561 FYVTETTFQKNRLFFYRKSVWSKLQSIGIRQHLKRVQLRELSEAEVRQHREARPALLTSR 620
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        601 FYVTETTFQKNRLFFYRKSVWSKLQSIGIRQHLKRVQLRELSEAEVRQHREARPALLTSR 660

Qy        621 LRFIPKPDGLRPIVNMDYVVGARTFRREKRAERLTSRVKALFSVLNYERARRPGLLGASV 680
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        661 LRFIPKPDGLRPIVNMDYVVGARTFRREKRAERLTSRVKALFSVLNYERARRPGLLGASV 720

Qy        681 LGLDDIHRAWRTFVLRVRAQDPPPELYFVKVDVTGAYDTIPQDRLTEVIASIIKPQNTYC 740
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        721 LGLDDIHRAWRTFVLRVRAQDPPPELYFVKVDVTGAYDTIPQDRLTEVIASIIKPQNTYC 780

Qy        741 VRRYAVVQKAAHGHVRKAFKSHVSTLTDLQPYMRQFVAHLQETSPLRDAVVIEQSSSLNE 800
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        781 VRRYAVVQKAAHGHVRKAFKSHVSTLTDLQPYMRQFVAHLQETSPLRDAVVIEQSSSLNE 840

Qy        801 ASSGLFDVFLRFMCHHAVRIRGKSYVQCQGIPQGSILSTLLCSLCYGDMENKLFAGIRRD 860
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        841 ASSGLFDVFLRFMCHHAVRIRGKSYVQCQGIPQGSILSTLLCSLCYGDMENKLFAGIRRD 900

Qy        861 GLLLRLVDDFLLVTPHLTHAKTFLRTLVRGVPEYGCVVNLRKTVVNFPVEDEALGGTAFV 920
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        901 GLLLRLVDDFLLVTPHLTHAKTFLRTLVRGVPEYGCVVNLRKTVVNFPVEDEALGGTAFV 960

Qy        921 QMPAHGLFPWCGLLLDTRTLEVQSDYSSYARTSIRASLTFNRGFKAGRNMRRKLFGVLRL 980
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        961 QMPAHGLFPWCGLLLDTRTLEVQSDYSSYARTSIRASLTFNRGFKAGRNMRRKLFGVLRL 1020

Qy        981 KCHSLFLDLQVNSLQTVCTNIYKILLLQAYRFHACVLQLPFHQQVWKNPTFFLRVISDTA 1040
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1021 KCHSLFLDLQVNSLQTVCTNIYKILLLQAYRFHACVLQLPFHQQVWKNPTFFLRVISDTA 1080

Qy       1041 SLCYSILKAKNA 1052
              ||||||||||||
Db       1081 SLCYSILKAKNA 1092


RESULT 41
AAY00652
ID   AAY00652 standard; protein; 1041 AA.
XX
AC   AAY00652;
XX
DT   26-JUL-1999  (first entry)
XX
DE   Altered C-terminus telomerase lacking motif A (ver. 2) protein sequence.
XX
KW   Telomerase; human; cancer; diagnosis; melanoma; skin cancer; leukaemia;
KW   neuroblastoma; breast carcinoma; colon carcinoma; lymphoma; osteosarcoma;
KW   smooth muscle cell hyperplasia; stem cell proliferation; Wilm's tumour;
KW   stem cell differentiation; organ regeneration; organ differentiation.
XX
OS   Homo sapiens.
OS   Synthetic.
XX
PN   WO9901560-A1.
XX
PD   14-JAN-1999.
XX
PF   01-JUL-1998;   98WO-US013835.
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XX
PR   01-JUL-1997;   97US-0051410P.
PR   21-JUL-1997;   97US-0053018P.
PR   21-JUL-1997;   97US-0053329P.
PR   04-AUG-1997;   97US-0054642P.
PR   09-SEP-1997;   97US-0058287P.
XX
PA   (CAMB-) CAMBIA BIOSYSTEMS LLC.
XX
PI   Kilian A,  Bowtell D;
XX
DR   WPI; 1999-106060/09.
DR   N-PSDB; AAX18280.
XX
PT   New isolated vertebrate telomerase genes - used to develop products for
PT   treating cancers or for organ regeneration, nerve cell or brain cell
PT   growth following injury or bone marrow transplantation.
XX
PS   Claim 4; Fig 11am-an; 134pp; English.
XX
CC   This sequence is a truncated human telomerase of the invention. Primers
CC   that amplify the telomerase coding sequence can be used in a method for
CC   diagnosing cancer in a patient. The telomerase can be used for detection,
CC   diagnosis and drug screening. Inhibitors of telomerase activity can be
CC   used to treat cancers such as melanomas, other skin cancers,
CC   neuroblastomas, breast carcinomas, colon carcinomas, leukaemias,
CC   lymphomas, osteosarcomas or smooth muscle cell hyperplasias or skin
CC   growths. Enhancers of telomerase may be used to stimulate stem cell
CC   proliferation and differentiation (expansion of haematopoietic stem cells
CC   could be administered in the bone marrow transplant context). As well,
CC   many tissues have stem cells. Proliferation of these cells may be useful
CC   in wound healing, hair growth, treatment of disease such as Wilm's
CC   tumour, organ regeneration or differentiation after injury or diseases,
CC   nerve cell or brain cell growth following injury. Note: The N-terminus of
CC   this sequence can be replaced by the sequences shown in AAY00656-Y00658,
CC   and the C-terminus can be replaced by the sequence shown in AAY00654
XX
SQ   Sequence 1041 AA;

  Query Match             91.7%;  Score 5467;  DB 2;  Length 1041;
  Best Local Similarity   98.8%;  Pred. No. 0;
  Matches 1039;  Conservative    0;  Mismatches    1;  Indels   12;  Gaps    1;

Qy          1 MPRAPRCRAVRSLLRSHYREVLPLATFVRRLGPQGWRLVQRGDPAAFRALVAQCLVCVPW 60
              |||||||||||||||| ||||||||||||||||||||||||||||||||||||||||||
Db          1 MPRAPRCRAVRSLLRSHTREVLPLATFVRRLGPQGWRLVQRGDPAAFRALVAQCLVCVPW 60

Qy         61 DARPPPAAPSFRQVSCLKELVARVLQRLCERGAKNVLAFGFALLDGARGGPPEAFTTSVR 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 DARPPPAAPSFRQVSCLKELVARVLQRLCERGAKNVLAFGFALLDGARGGPPEAFTTSVR 120

Qy        121 SYLPNTVTDALRGSGAWGLLLRRVGDDVLVHLLARCALFVLVAPSCAYQVCGPPLYQLGA 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 SYLPNTVTDALRGSGAWGLLLRRVGDDVLVHLLARCALFVLVAPSCAYQVCGPPLYQLGA 180

Qy        181 ATQARPPPHASGPRRRLGCERAWNHSVREAGVPLGLPAPGARRRGGSASRSLPLPKRPRR 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 ATQARPPPHASGPRRRLGCERAWNHSVREAGVPLGLPAPGARRRGGSASRSLPLPKRPRR 240

Qy        241 GAAPEPERTPVGQGSWAHPGRTRGPSDRGFCVVSPARPAEEATSLEGALSGTRHSHPSVG 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 GAAPEPERTPVGQGSWAHPGRTRGPSDRGFCVVSPARPAEEATSLEGALSGTRHSHPSVG 300

Qy        301 RQHHAGPPSTSRPPRPWDTPCPPVYAETKHFLYSSGDKEQLRPSFLLSSLRPSLTGARRL 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 RQHHAGPPSTSRPPRPWDTPCPPVYAETKHFLYSSGDKEQLRPSFLLSSLRPSLTGARRL 360

Qy        361 VETIFLGSRPWMPGTPRRLPRLPQRYWQMRPLFLELLGNHAQCPYGVLLKTHCPLRAAVT 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        361 VETIFLGSRPWMPGTPRRLPRLPQRYWQMRPLFLELLGNHAQCPYGVLLKTHCPLRAAVT 420

Qy        421 PAAGVCAREKPQGSVAAPEEEDTDPRRLVQLLRQHSSPWQVYGFVRACLRRLVPPGLWGS 480
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        421 PAAGVCAREKPQGSVAAPEEEDTDPRRLVQLLRQHSSPWQVYGFVRACLRRLVPPGLWGS 480

Qy        481 RHNERRFLRNTKKFISLGKHAKLSLQELTWKMSVRDCAWLRRSPGVGCVPAAEHRLREEI 540
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        481 RHNERRFLRNTKKFISLGKHAKLSLQELTWKMSVRDCAWLRRSPGVGCVPAAEHRLREEI 540

Qy        541 LAKFLHWLMSVYVVELLRSFFYVTETTFQKNRLFFYRKSVWSKLQSIGIRQHLKRVQLRE 600
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        541 LAKFLHWLMSVYVVELLRSFFYVTETTFQKNRLFFYRKSVWSKLQSIGIRQHLKRVQLRE 600

Qy        601 LSEAEVRQHREARPALLTSRLRFIPKPDGLRPIVNMDYVVGARTFRREKRAERLTSRVKA 660
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        601 LSEAEVRQHREARPALLTSRLRFIPKPDGLRPIVNMDYVVGARTFRREKRAERLTSRVKA 660

Qy        661 LFSVLNYERARRPGLLGASVLGLDDIHRAWRTFVLRVRAQDPPPELYFVKVDVTGAYDTI 720
              ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        661 LFSVLNYERARRPGLLGASVLGLDDIHRAWRTFVLRVRAQDPPPELYFVK---------- 710

Qy        721 PQDRLTEVIASIIKPQNTYCVRRYAVVQKAAHGHVRKAFKSHVSTLTDLQPYMRQFVAHL 780
                  ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        711 --DRLTEVIASIIKPQNTYCVRRYAVVQKAAHGHVRKAFKSHVSTLTDLQPYMRQFVAHL 768

Qy        781 QETSPLRDAVVIEQSSSLNEASSGLFDVFLRFMCHHAVRIRGKSYVQCQGIPQGSILSTL 840
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        769 QETSPLRDAVVIEQSSSLNEASSGLFDVFLRFMCHHAVRIRGKSYVQCQGIPQGSILSTL 828

Qy        841 LCSLCYGDMENKLFAGIRRDGLLLRLVDDFLLVTPHLTHAKTFLRTLVRGVPEYGCVVNL 900
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        829 LCSLCYGDMENKLFAGIRRDGLLLRLVDDFLLVTPHLTHAKTFLRTLVRGVPEYGCVVNL 888

Qy        901 RKTVVNFPVEDEALGGTAFVQMPAHGLFPWCGLLLDTRTLEVQSDYSSYARTSIRASLTF 960
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        889 RKTVVNFPVEDEALGGTAFVQMPAHGLFPWCGLLLDTRTLEVQSDYSSYARTSIRASLTF 948

Qy        961 NRGFKAGRNMRRKLFGVLRLKCHSLFLDLQVNSLQTVCTNIYKILLLQAYRFHACVLQLP 1020
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        949 NRGFKAGRNMRRKLFGVLRLKCHSLFLDLQVNSLQTVCTNIYKILLLQAYRFHACVLQLP 1008

Qy       1021 FHQQVWKNPTFFLRVISDTASLCYSILKAKNA 1052
              ||||||||||||||||||||||||||||||||
Db       1009 FHQQVWKNPTFFLRVISDTASLCYSILKAKNA 1040


RESULT 42
AAY00643
ID   AAY00643 standard; protein; 1041 AA.
XX
AC   AAY00643;
XX
DT   26-JUL-1999  (first entry)
XX
DE   Altered C-terminused telomerase protein sequence lacking motif A.
XX
KW   Telomerase; human; cancer; diagnosis; melanoma; skin cancer; leukaemia;
KW   neuroblastoma; breast carcinoma; colon carcinoma; lymphoma; osteosarcoma;
KW   smooth muscle cell hyperplasia; stem cell proliferation; Wilm's tumour;
KW   stem cell differentiation; organ regeneration; organ differentiation.
XX
OS   Homo sapiens.
OS   Synthetic.
XX
PN   WO9901560-A1.
XX
PD   14-JAN-1999.
XX
PF   01-JUL-1998;   98WO-US013835.
XX
PR   01-JUL-1997;   97US-0051410P.
PR   21-JUL-1997;   97US-0053018P.
PR   21-JUL-1997;   97US-0053329P.
PR   04-AUG-1997;   97US-0054642P.
PR   09-SEP-1997;   97US-0058287P.
XX
```

```
PA   (CAMB-) CAMBIA BIOSYSTEMS LLC.
XX
PI   Kilian A,  Bowtell D;
XX
DR   WPI; 1999-106060/09.
DR   N-PSDB; AAX18271.
XX
PT   New isolated vertebrate telomerase genes - used to develop products for
PT   treating cancers or for organ regeneration, nerve cell or brain cell
PT   growth following injury or bone marrow transplantation.
XX
PS   Claim 4; Fig 11r-s; 134pp; English.
XX
CC   This sequence is a truncated human telomerase of the invention. Primers
CC   that amplify the telomerase coding sequence can be used in a method for
CC   diagnosing cancer in a patient. The telomerase can be used for detection,
CC   diagnosis and drug screening. Inhibitors of telomerase activity can be
CC   used to treat cancers such as melanomas, other skin cancers,
CC   neuroblastomas, breast carcinomas, colon carcinomas, leukaemias,
CC   lymphomas, osteosarcomas or smooth muscle cell hyperplasias or skin
CC   growths. Enhancers of telomerase may be used to stimulate stem cell
CC   proliferation and differentiation (expansion of haematopoietic stem cells
CC   could be administered in the bone marrow transplant context). As well,
CC   many tissues have stem cells. Proliferation of these cells may be useful
CC   in wound healing, hair growth, treatment of disease such as Wilm's
CC   tumour, organ regeneration or differentiation after injury or diseases,
CC   nerve cell or brain cell growth following injury. Note: The C-terminus of
CC   this sequence can be replaced by the sequence shown in AAY00654
XX
SQ   Sequence 1041 AA;

  Query Match             91.7%;  Score 5467;  DB 2;  Length 1041;
  Best Local Similarity   98.8%;  Pred. No. 0;
  Matches 1039;  Conservative    0;  Mismatches    1;  Indels   12;  Gaps    1;

Qy          1 MPRAPRCRAVRSLLRSHYREVLPLATFVRRLGPQGWRLVQRGDPAAFRALVAQCLVCVPW 60
              ||||||||||||||||| |||||||||||||||||||||||||||||||||||||||||
Db          1 MPRAPRCRAVRSLLRSHTREVLPLATFVRRLGPQGWRLVQRGDPAAFRALVAQCLVCVPW 60

Qy         61 DARPPPAAPSFRQVSCLKELVARVLQRLCERGAKNVLAFGFALLDGARGGPPEAFTTSVR 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 DARPPPAAPSFRQVSCLKELVARVLQRLCERGAKNVLAFGFALLDGARGGPPEAFTTSVR 120

Qy        121 SYLPNTVTDALRGSGAWGLLLRRVGDDVLVHLLARCALFVLVAPSCAYQVCGPPLYQLGA 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 SYLPNTVTDALRGSGAWGLLLRRVGDDVLVHLLARCALFVLVAPSCAYQVCGPPLYQLGA 180

Qy        181 ATQARPPPHASGPRRRLGCERAWNHSVREAGVPLGLPAPGARRRGGSASRSLPLPKRPRR 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 ATQARPPPHASGPRRRLGCERAWNHSVREAGVPLGLPAPGARRRGGSASRSLPLPKRPRR 240

Qy        241 GAAPEPERTPVGQGSWAHPGRTRGPSDRGFCVVSPARPAEEATSLEGALSGTRHSHPSVG 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 GAAPEPERTPVGQGSWAHPGRTRGPSDRGFCVVSPARPAEEATSLEGALSGTRHSHPSVG 300

Qy        301 RQHHAGPPSTSRPPRPWDTPCPPVYAETKHFLYSSGDKEQLRPSFLLSSLRPSLTGARRL 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 RQHHAGPPSTSRPPRPWDTPCPPVYAETKHFLYSSGDKEQLRPSFLLSSLRPSLTGARRL 360

Qy        361 VETIFLGSRPWMPGTPRRLPRLPQRYWQMRPLFLELLGNHAQCPYGVLLKTHCPLRAAVT 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        361 VETIFLGSRPWMPGTPRRLPRLPQRYWQMRPLFLELLGNHAQCPYGVLLKTHCPLRAAVT 420

Qy        421 PAAGVCAREKPQGSVAAPEEEDTDPRRLVQLLRQHSSPWQVYGFVRACLRRLVPPGLWGS 480
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        421 PAAGVCAREKPQGSVAAPEEEDTDPRRLVQLLRQHSSPWQVYGFVRACLRRLVPPGLWGS 480

Qy        481 RHNERRFLRNTKKFISLGKHAKLSLQELTWKMSVRDCAWLRRSPGVGCVPAAEHRLREEI 540
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        481 RHNERRFLRNTKKFISLGKHAKLSLQELTWKMSVRDCAWLRRSPGVGCVPAAEHRLREEI 540

Qy        541 LAKFLHWLMSVYVVELLRSFFYVTETTFQKNRLFFYRKSVWSKLQSIGIRQHLKRVQLRE 600
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        541 LAKFLHWLMSVYVVELLRSFFYVTETTFQKNRLFFYRKSVWSKLQSIGIRQHLKRVQLRE 600

Qy        601 LSEAEVRQHREARPALLTSRLRFIPKPDGLRPIVNMDYVVGARTFRREKRAERLTSRVKA 660
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        601 LSEAEVRQHREARPALLTSRLRFIPKPDGLRPIVNMDYVVGARTFRREKRAERLTSRVKA 660

Qy        661 LFSVLNYERARRPGLLGASVLGLDDIHRAWRTFVLRVRAQDPPPELYFVKVDVTGAYDTI 720
              ||||||||||||||||||||||||||||||||||||||||||||||||||
Db        661 LFSVLNYERARRPGLLGASVLGLDDIHRAWRTFVLRVRAQDPPPELYFVK---------- 710

Qy        721 PQDRLTEVIASIIKPQNTYCVRRYAVVQKAAHGHVRKAFKSHVSTLTDLQPYMRQFVAHL 780
                  ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        711 --DRLTEVIASIIKPQNTYCVRRYAVVQKAAHGHVRKAFKSHVSTLTDLQPYMRQFVAHL 768

Qy        781 QETSPLRDAVVIEQSSSLNEASSGLFDVFLRFMCHHAVRIRGKSYVQCQGIPQGSILSTL 840
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        769 QETSPLRDAVVIEQSSSLNEASSGLFDVFLRFMCHHAVRIRGKSYVQCQGIPQGSILSTL 828

Qy        841 LCSLCYGDMENKLFAGIRRDGLLLRLVDDFLLVTPHLTHAKTFLRTLVRGVPEYGCVVNL 900
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        829 LCSLCYGDMENKLFAGIRRDGLLLRLVDDFLLVTPHLTHAKTFLRTLVRGVPEYGCVVNL 888

Qy        901 RKTVVNFPVEDEALGGTAFVQMPAHGLFPWCGLLLDTRTLEVQSDYSSYARTSIRASLTF 960
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        889 RKTVVNFPVEDEALGGTAFVQMPAHGLFPWCGLLLDTRTLEVQSDYSSYARTSIRASLTF 948

Qy        961 NRGFKAGRNMRRKLFGVLRLKCHSLFLDLQVNSLQTVCTNIYKILLLQAYRFHACVLQLP 1020
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        949 NRGFKAGRNMRRKLFGVLRLKCHSLFLDLQVNSLQTVCTNIYKILLLQAYRFHACVLQLP 1008

Qy       1021 FHQQVWKNPTFFLRVISDTASLCYSILKAKNA 1052
              ||||||||||||||||||||||||||||||||
Db       1009 FHQQVWKNPTFFLRVISDTASLCYSILKAKNA 1040


RESULT 43
AAY00639
ID   AAY00639 standard; protein; 948 AA.
XX
AC   AAY00639;
XX
DT   26-JUL-1999  (first entry)
XX
DE   N-terminal truncated telomerase protein sequence.
XX
KW   Telomerase; human; cancer; diagnosis; melanoma; skin cancer; leukaemia;
KW   neuroblastoma; breast carcinoma; colon carcinoma; lymphoma; osteosarcoma;
KW   smooth muscle cell hyperplasia; stem cell proliferation; Wilm's tumour;
KW   stem cell differentiation; organ regeneration; organ differentiation.
XX
OS   Homo sapiens.
OS   Synthetic.
XX
PN   WO9901560-A1.
XX
PD   14-JAN-1999.
XX
PF   01-JUL-1998;   98WO-US013835.
XX
PR   01-JUL-1997;   97US-0051410P.
PR   21-JUL-1997;   97US-0053018P.
PR   21-JUL-1997;   97US-0053329P.
PR   04-AUG-1997;   97US-0054642P.
PR   09-SEP-1997;   97US-0058287P.
XX
PA   (CAMB-) CAMBIA BIOSYSTEMS LLC.
XX
PI   Kilian A,  Bowtell D;
XX
DR   WPI; 1999-106060/09.
DR   N-PSDB; AAY00639.
XX
PT   New isolated vertebrate telomerase genes - used to develop products for
```

PT treating cancers or for organ regeneration, nerve cell or brain cell
PT growth following injury or bone marrow transplantation.
XX
PS Claim 4; Fig 11j-k; 134pp; English.
XX
CC This sequence is a truncated human telomerase of the invention. Primers
CC that amplify the telomerase coding sequence can be used in a method for
CC diagnosing cancer in a patient. The telomerase can be used for detection,
CC diagnosis and drug screening. Inhibitors of telomerase activity can be
CC used to treat cancers such as melanomas, other skin cancers,
CC neuroblastomas, breast carcinomas, colon carcinomas, leukaemias,
CC lymphomas, osteosarcomas or smooth muscle cell hyperplasias or skin
CC growths. Enhancers of telomerase may be used to stimulate stem cell
CC proliferation and differentiation (expansion of haematopoietic stem cells
CC could be administered in the bone marrow transplant context). As well,
CC many tissues have stem cells. Proliferation of these cells may be useful
CC in wound healing, hair growth, treatment of disease such as Wilm's
CC tumour, organ regeneration or differentiation after injury or diseases,
CC nerve cell or brain cell growth following injury
XX
SQ Sequence 948 AA;

Query Match 84.0%; Score 5008; DB 2; Length 948;
Best Local Similarity 99.9%; Pred. No. 0;
Matches 946; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

```
Qy          1 MPRAPRCRAVRSLLRSHYREVLPLATFVRRLGPQGWRLVQRGDPAAFRALVAQCLVCVPW 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 MPRAPRCRAVRSLLRSHYREVLPLATFVRRLGPQGWRLVQRGDPAAFRALVAQCLVCVPW 60

Qy         61 DARPPPAAPSFRQVSCLKELVARVLQRLCERGAKNVLAFGFALLDGARGGPPEAFTTSVR 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 DARPPPAAPSFRQVSCLKELVARVLQRLCERGAKNVLAFGFALLDGARGGPPEAFTTSVR 120

Qy        121 SYLPNTVTDALRGSGAWGLLLRRVGDDVLVHLLARCALFVLVAPSCAYQVCGPPLYQLGA 180
              |||||||||||||:||||||||||||||||||||||||||||||||||||||||||||||
Db        121 SYLPNTVTDALRGTGAWGLLLRRVGDDVLVHLLARCALFVLVAPSCAYQVCGPPLYQLGA 180

Qy        181 ATQARPPPHASGPRRRLGCERAWNHSVREAGVPLGLPAPGARRRGGSASRSLPLPKRPRR 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 ATQARPPPHASGPRRRLGCERAWNHSVREAGVPLGLPAPGARRRGGSASRSLPLPKRPRR 240

Qy        241 GAAPEPERTPVGQGSWAHPGRTRGPSDRGFCVVSPARPAEEATSLEGALSGTRHSHPSVG 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 GAAPEPERTPVGQGSWAHPGRTRGPSDRGFCVVSPARPAEEATSLEGALSGTRHSHPSVG 300

Qy        301 RQHHAGPPSTSRPPRPWDTPCPPVYAETKHFLYSSGDKEQLRPSFLLSSLRPSLTGARRL 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 RQHHAGPPSTSRPPRPWDTPCPPVYAETKHFLYSSGDKEQLRPSFLLSSLRPSLTGARRL 360

Qy        361 VETIFLGSRPWMPGTPRRLPRLPQRYWQMRPLFLELLGNHAQCPYGVLLKTHCPLRAAVT 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        361 VETIFLGSRPWMPGTPRRLPRLPQRYWQMRPLFLELLGNHAQCPYGVLLKTHCPLRAAVT 420

Qy        421 PAAGVCAREKPQGSVAAPEEEDTDPRRLVQLLRQHSSPWQVYGFVRACLRRLVPPGLWGS 480
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        421 PAAGVCAREKPQGSVAAPEEEDTDPRRLVQLLRQHSSPWQVYGFVRACLRRLVPPGLWGS 480

Qy        481 RHNERRFLRNTKKFISLGKHAKLSLQELTWKMSVRDCAWLRRSPGVGCVPAAEHRLREEI 540
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        481 RHNERRFLRNTKKFISLGKHAKLSLQELTWKMSVRDCAWLRRSPGVGCVPAAEHRLREEI 540

Qy        541 LAKFLHWLMSVYVVELLRSFFYVTETTFQKNRLFFYRKSVWSKLQSIGIRQHLKRVQLRE 600
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        541 LAKFLHWLMSVYVVELLRSFFYVTETTFQKNRLFFYRKSVWSKLQSIGIRQHLKRVQLRE 600

Qy        601 LSEAEVRQHREARPALLTSRLRFIPKPDGLRPIVNMDYVVGARTFRREKRAERLTSRVKA 660
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        601 LSEAEVRQHREARPALLTSRLRFIPKPDGLRPIVNMDYVVGARTFRREKRAERLTSRVKA 660

Qy        661 LFSVLNYERARRPGLLGASVLGLDDIHRAWRTFVLRVRAQDPPPELYFVKVDVTGAYDTI 720
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        661 LFSVLNYERARRPGLLGASVLGLDDIHRAWRTFVLRVRAQDPPPELYFVKVDVTGAYDTI 720

Qy        721 PQDRLTEVIASIIKPQNTYCVRRYAVVQKAAHGHVRKAFKSHVSTLTDLQPYMRQFVAHL 780
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        721 PQDRLTEVIASIIKPQNTYCVRRYAVVQKAAHGHVRKAFKSHVSTLTDLQPYMRQFVAHL 780

Qy        781 QETSPLRDAVVIEQSSSLNEASSGLFDVFLRFMCHHAVRIRGKSYVQCQGIPQGSILSTL 840
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        781 QETSPLRDAVVIEQSSSLNEASSGLFDVFLRFMCHHAVRIRGKSYVQCQGIPQGSILSTL 840

Qy        841 LCSLCYGDMENKLFAGIRRDGLLLRLVDDFLLVTPHLTHAKTFLRTLVRGVPEYGCVVNL 900
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        841 LCSLCYGDMENKLFAGIRRDGLLLRLVDDFLLVTPHLTHAKTFLRTLVRGVPEYGCVVNL 900

Qy        901 RKTVVNFPVEDEALGGTAFVQMPAHGLFPWCGLLLDTRTLEVQSDYS 947
              |||||||||||||||||||||||||||||||||||||||||||||||
Db        901 RKTVVNFPVEDEALGGTAFVQMPAHGLFPWCGLLLDTRTLEVQSDYS 947
```

RESULT 44
AAY00648
ID AAY00648 standard; protein; 948 AA.
XX
AC AAY00648;
XX
DT 26-JUL-1999 (first entry)
XX
DE Truncated telomerase 3 protein sequence.
XX
KW Telomerase; human; cancer; diagnosis; melanoma; skin cancer; leukaemia;
KW neuroblastoma; breast carcinoma; colon carcinoma; lymphoma; osteosarcoma;
KW smooth muscle cell hyperplasia; stem cell proliferation; Wilm's tumour;
KW stem cell differentiation; organ regeneration; organ differentiation.
XX
OS Homo sapiens.
OS Synthetic.
XX
PN WO9901560-A1.
XX
PD 14-JAN-1999.
XX
PF 01-JUL-1998; 98WO-US013835.
XX
PR 01-JUL-1997; 97US-0051410P.
PR 21-JUL-1997; 97US-0053018P.
PR 21-JUL-1997; 97US-0053329P.
PR 04-AUG-1997; 97US-0054642P.
PR 09-SEP-1997; 97US-0058287P.
XX
PA (CAMB-) CAMBIA BIOSYSTEMS LLC.
XX
PI Kilian A, Bowtell D;
XX
DR WPI; 1999-106060/09.
DR N-PSDB; AAX18276.
XX
PT New isolated vertebrate telomerase genes - used to develop products for
PT treating cancers or for organ regeneration, nerve cell or brain cell
PT growth following injury or bone marrow transplantation.
XX
PS Claim 4; Fig 11ad-ae; 134pp; English.
XX
CC This sequence is a truncated human telomerase of the invention. Primers
CC that amplify the telomerase coding sequence can be used in a method for
CC diagnosing cancer in a patient. The telomerase can be used for detection,
CC diagnosis and drug screening. Inhibitors of telomerase activity can be
CC used to treat cancers such as melanomas, other skin cancers,
CC neuroblastomas, breast carcinomas, colon carcinomas, leukaemias,
CC lymphomas, osteosarcomas or smooth muscle cell hyperplasias or skin
CC growths. Enhancers of telomerase may be used to stimulate stem cell
CC proliferation and differentiation (expansion of haematopoietic stem cells
CC could be administered in the bone marrow transplant context). As well,
CC many tissues have stem cells. Proliferation of these cells may be useful
CC in wound healing, hair growth, treatment of disease such as Wilm's

```
CC   tumour, organ regeneration or differentiation after injury or diseases,
CC   nerve cell or brain cell growth following injury. Note: The N-terminus of
CC   this sequence can be replaced by the sequences shown in AAY00656-Y00658
XX
SQ   Sequence 948 AA;

  Query Match           83.9%;  Score 5004;  DB 2;  Length 948;
  Best Local Similarity  99.9%;  Pred. No. 0;
  Matches  946;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          1 MPRAPRCRAVRSLLRSHYREVLPLATFVRRLGPQGWRLVQRGDPAAFRALVAQCLVCVPW 60
              ||||||||| |||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 MPRAPRCRAVPSLLRSHYREVLPLATFVRRLGPQGWRLVQRGDPAAFRALVAQCLVCVPW 60

Qy         61 DARPPPAAPSFRQVSCLKELVARVLQRLCERGAKNVLAFGFALLDGARGGPPEAFTTSVR 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 DARPPPAAPSFRQVSCLKELVARVLQRLCERGAKNVLAFGFALLDGARGGPPEAFTTSVR 120

Qy        121 SYLPNTVTDALRGSGAWGLLLRRVGDDVLVHLLARCALFVLVAPSCAYQVCGPPLYQLGA 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 SYLPNTVTDALRGSGAWGLLLRRVGDDVLVHLLARCALFVLVAPSCAYQVCGPPLYQLGA 180

Qy        181 ATQARPPPHASGPRRRLGCERAWNHSVREAGVPLGLPAPGARRRGGSASRSLPLPKRPRR 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 ATQARPPPHASGPRRRLGCERAWNHSVREAGVPLGLPAPGARRRGGSASRSLPLPKRPRR 240

Qy        241 GAAPEPERTPVGQGSWAHPGRTRGPSDRGFCVVSPARPAEEATSLEGALSGTRHSHPSVG 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 GAAPEPERTPVGQGSWAHPGRTRGPSDRGFCVVSPARPAEEATSLEGALSGTRHSHPSVG 300

Qy        301 RQHHAGPPSTSRPPRPWDTPCPPVYAETKHFLYSSGDKEQLRPSFLLSSLRPSLTGARRL 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 RQHHAGPPSTSRPPRPWDTPCPPVYAETKHFLYSSGDKEQLRPSFLLSSLRPSLTGARRL 360

Qy        361 VETIFLGSRPWMPGTPRRLPRLPQRYWQMRPLFLELLGNHAQCPYGVLLKTHCPLRAAVT 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        361 VETIFLGSRPWMPGTPRRLPRLPQRYWQMRPLFLELLGNHAQCPYGVLLKTHCPLRAAVT 420

Qy        421 PAAGVCAREKPQGSVAAPEEEDTDPRRLVQLLRQHSSPWQVYGFVRACLRRLVPPGLWGS 480
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        421 PAAGVCAREKPQGSVAAPEEEDTDPRRLVQLLRQHSSPWQVYGFVRACLRRLVPPGLWGS 480

Qy        481 RHNERRFLRNTKKFISLGKHAKLSLQELTWKMSVRDCAWLRRSPGVGCVPAAEHRLREEI 540
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        481 RHNERRFLRNTKKFISLGKHAKLSLQELTWKMSVRDCAWLRRSPGVGCVPAAEHRLREEI 540

Qy        541 LAKFLHWLMSVYVVELLRSFFYVTETTFQKNRLFFYRKSVWSKLQSIGIRQHLKRVQLRE 600
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        541 LAKFLHWLMSVYVVELLRSFFYVTETTFQKNRLFFYRKSVWSKLQSIGIRQHLKRVQLRE 600

Qy        601 LSEAEVRQHREARPALLTSRLRFIPKPDGLRPIVNMDYVVGARTFRREKRAERLTSRVKA 660
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        601 LSEAEVRQHREARPALLTSRLRFIPKPDGLRPIVNMDYVVGARTFRREKRAERLTSRVKA 660

Qy        661 LFSVLNYERARRPGLLGASVLGLDDIHRAWRTFVLRVRAQDPPPELYFVKVDVTGAYDTI 720
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        661 LFSVLNYERARRPGLLGASVLGLDDIHRAWRTFVLRVRAQDPPPELYFVKVDVTGAYDTI 720

Qy        721 PQDRLTEVIASIIKPQNTYCVRRYAVVQKAAHGHVRKAFKSHVSTLTDLQPYMRQFVAHL 780
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        721 PQDRLTEVIASIIKPQNTYCVRRYAVVQKAAHGHVRKAFKSHVSTLTDLQPYMRQFVAHL 780

Qy        781 QETSPLRDAVVIEQSSSLNEASSGLFDVFLRFMCHHAVRIRGKSYVQCQGIPQGSILSTL 840
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        781 QETSPLRDAVVIEQSSSLNEASSGLFDVFLRFMCHHAVRIRGKSYVQCQGIPQGSILSTL 840

Qy        841 LCSLCYGDMENKLFAGIRRDGLLLRLVDDFLLVTPHLTHAKTFLRTLVRGVPEYGCVVNL 900
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        841 LCSLCYGDMENKLFAGIRRDGLLLRLVDDFLLVTPHLTHAKTFLRTLVRGVPEYGCVVNL 900

Qy        901 RKTVVNFPVEDEALGGTAFVQMPAHGLFPWCGLLLDTRTLEVQSDYS 947
              |||||||||||||||||||||||||||||||||||||||||||||||
Db        901 RKTVVNFPVEDEALGGTAFVQMPAHGLFPWCGLLLDTRTLEVQSDYS 947
```

```
RESULT 45
AAY00642
ID   AAY00642 standard; protein; 936 AA.
XX
AC   AAY00642;
XX
DT   26-JUL-1999  (first entry)
XX
DE   Truncated telomerase protein sequence lacking motif A.
XX
KW   Telomerase; human; cancer; diagnosis; melanoma; skin cancer; leukaemia;
KW   neuroblastoma; breast carcinoma; colon carcinoma; lymphoma; osteosarcoma;
KW   smooth muscle cell hyperplasia; stem cell proliferation; Wilm's tumour;
KW   stem cell differentiation; organ regeneration; organ differentiation.
XX
OS   Homo sapiens.
OS   Synthetic.
XX
PN   WO9901560-A1.
XX
PD   14-JAN-1999.
XX
PF   01-JUL-1998;   98WO-US013835.
XX
PR   01-JUL-1997;   97US-0051410P.
PR   21-JUL-1997;   97US-0053018P.
PR   21-JUL-1997;   97US-0053329P.
PR   04-AUG-1997;   97US-0054642P.
PR   09-SEP-1997;   97US-0058287P.
XX
PA   (CAMB-) CAMBIA BIOSYSTEMS LLC.
XX
PI   Kilian A,  Bowtell D;
XX
DR   WPI; 1999-106060/09.
DR   N-PSDB; AAX18270.
XX
PT   New isolated vertebrate telomerase genes - used to develop products for
PT   treating cancers or for organ regeneration, nerve cell or brain cell
PT   growth following injury or bone marrow transplantation.
XX
PS   Claim 4; Fig 11p-q; 134pp; English.
XX
CC   This sequence is a truncated human telomerase of the invention. Primers
CC   that amplify the telomerase coding sequence can be used in a method for
CC   diagnosing cancer in a patient. The telomerase can be used for detection,
CC   diagnosis and drug screening. Inhibitors of telomerase activity can be
CC   used to treat cancers such as melanomas, other skin cancers,
CC   neuroblastomas, breast carcinomas, colon carcinomas, leukaemias,
CC   lymphomas, osteosarcomas or smooth muscle cell hyperplasias or skin
CC   growths. Enhancers of telomerase may be used to stimulate stem cell
CC   proliferation and differentiation (expansion of haematopoietic stem cells
CC   could be administered in the bone marrow transplant context). As well,
CC   many tissues have stem cells. Proliferation of these cells may be useful
CC   in wound healing, hair growth, treatment of disease such as Wilm's
CC   tumour, organ regeneration or differentiation after injury or diseases,
CC   nerve cell or brain cell growth following injury
XX
SQ   Sequence 936 AA;

  Query Match           82.7%;  Score 4932;  DB 2;  Length 936;
  Best Local Similarity  98.7%;  Pred. No. 0;
  Matches  935;  Conservative    0;  Mismatches    0;  Indels   12;  Gaps    1;

Qy          1 MPRAPRCRAVRSLLRSHYREVLPLATFVRRLGPQGWRLVQRGDPAAFRALVAQCLVCVPW 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 MPRAPRCRAVRSLLRSHYREVLPLATFVRRLGPQGWRLVQRGDPAAFRALVAQCLVCVPW 60

Qy         61 DARPPPAAPSFRQVSCLKELVARVLQRLCERGAKNVLAFGFALLDGARGGPPEAFTTSVR 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 DARPPPAAPSFRQVSCLKELVARVLQRLCERGAKNVLAFGFALLDGARGGPPEAFTTSVR 120
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```
Qy        121 SYLPNTVTDALRGSGAWGLLLRRVGDDVLVHLLARCALFVLVAPSCAYQVCGPPLYQLGA 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 SYLPNTVTDALRGSGAWGLLLRRVGDDVLVHLLARCALFVLVAPSCAYQVCGPPLYQLGA 180

Qy        181 ATQARPPPHASGPRRRLGCERAWNHSVREAGVPLGLPAPGARRRGGSASRSLPLPKRPRR 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 ATQARPPPHASGPRRRLGCERAWNHSVREAGVPLGLPAPGARRRGGSASRSLPLPKRPRR 240

Qy        241 GAAPEPERTPVGQGSWAHPGRTRGPSDRGFCVVSPARPAEEATSLEGALSGTRHSHPSVG 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 GAAPEPERTPVGQGSWAHPGRTRGPSDRGFCVVSPARPAEEATSLEGALSGTRHSHPSVG 300

Qy        301 RQHHAGPPSTSRPPRPWDTPCPPVYAETKHFLYSSGDKEQLRPSFLLSSLRPSLTGARRL 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 RQHHAGPPSTSRPPRPWDTPCPPVYAETKHFLYSSGDKEQLRPSFLLSSLRPSLTGARRL 360

Qy        361 VETIFLGSRPWMPGTPRRLPRLPQRYWQMRPLFLELLGNHAQCPYGVLLKTHCPLRAAVT 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        361 VETIFLGSRPWMPGTPRRLPRLPQRYWQMRPLFLELLGNHAQCPYGVLLKTHCPLRAAVT 420

Qy        421 PAAGVCAREKPQGSVAAPEEEDTDPRRLVQLLRQHSSPWQVYGFVRACLRRLVPPGLWGS 480
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        421 PAAGVCAREKPQGSVAAPEEEDTDPRRLVQLLRQHSSPWQVYGFVRACLRRLVPPGLWGS 480

Qy        481 RHNERRFLRNTKKFISLGKHAKLSLQELTWKMSVRDCAWLRRSPGVGCVPAAEHRLREEI 540
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        481 RHNERRFLRNTKKFISLGKHAKLSLQELTWKMSVRDCAWLRRSPGVGCVPAAEHRLREEI 540

Qy        541 LAKFLHWLMSVYVVELLRSFFYVTETTFQKNRLFFYRKSVWSKLQSIGIRQHLKRVQLRE 600
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        541 LAKFLHWLMSVYVVELLRSFFYVTETTFQKNRLFFYRKSVWSKLQSIGIRQHLKRVQLRE 600

Qy        601 LSEAEVRQHREARPALLTSRLRFIPKPDGLRPIVNMDYVVGARTFRREKRAERLTSRVKA 660
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        601 LSEAEVRQHREARPALLTSRLRFIPKPDGLRPIVNMDYVVGARTFRREKRAERLTSRVKA 660

Qy        661 LFSVLNYERARRPGLLGASVLGLDDIHRAWRTFVLRVRAQDPPPELYFVKVDVTGAYDTI 720
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        661 LFSVLNYERARRPGLLGASVLGLDDIHRAWRTFVLRVRAQDPPPELYFVK---------- 710

Qy        721 PQDRLTEVIASIIKPQNTYCVRRYAVVQKAAHGHVRKAFKSHVSTLTDLQPYMRQFVAHL 780
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        711 --DRLTEVIASIIKPQNTYCVRRYAVVQKAAHGHVRKAFKSHVSTLTDLQPYMRQFVAHL 768

Qy        781 QETSPLRDAVVIEQSSSLNEASSGLFDVFLRFMCHHAVRIRGKSYVQCQGIPQGSILSTL 840
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        769 QETSPLRDAVVIEQSSSLNEASSGLFDVFLRFMCHHAVRIRGKSYVQCQGIPQGSILSTL 828

Qy        841 LCSLCYGDMENKLFAGIRRDGLLLRLVDDFLLVTPHLTHAKTFLRTLVRGVPEYGCVVNL 900
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        829 LCSLCYGDMENKLFAGIRRDGLLLRLVDDFLLVTPHLTHAKTFLRTLVRGVPEYGCVVNL 888

Qy        901 RKTVVNFPVEDEALGGTAFVQMPAHGLFPWCGLLLDTRTLEVQSDYS 947
              |||||||||||||||||||||||||||||||||||||||||||||||
Db        889 RKTVVNFPVEDEALGGTAFVQMPAHGLFPWCGLLLDTRTLEVQSDYS 935


RESULT 46
AAY00651
ID   AAY00651 standard; protein; 936 AA.
XX
AC   AAY00651;
XX
DT   26-JUL-1999  (first entry)
XX
DE   Truncated telomerase (ver. 2) protein sequence lacking motif A.
XX
KW   Telomerase; human; cancer; diagnosis; melanoma; skin cancer; leukaemia;
KW   neuroblastoma; breast carcinoma; colon carcinoma; lymphoma; osteosarcoma;
KW   smooth muscle cell hyperplasia; stem cell proliferation; Wilm's tumour;
KW   stem cell differentiation; organ regeneration; organ differentiation.
XX
OS   Homo sapiens.
OS   Synthetic.
XX
PN   WO9901560-A1.
XX
PD   14-JAN-1999.
XX
PF   01-JUL-1998;   98WO-US013835.
XX
PR   01-JUL-1997;   97US-0051410P.
PR   21-JUL-1997;   97US-0053018P.
PR   21-JUL-1997;   97US-0053329P.
PR   04-AUG-1997;   97US-0054642P.
PR   09-SEP-1997;   97US-0058287P.
XX
PA   (CAMB-) CAMBIA BIOSYSTEMS LLC.
XX
PI   Kilian A,  Bowtell D;
XX
DR   WPI; 1999-106060/09.
DR   N-PSDB; AAX18279.
XX
PT   New isolated vertebrate telomerase genes - used to develop products for
PT   treating cancers or for organ regeneration, nerve cell or brain cell
PT   growth following injury or bone marrow transplantation.
XX
PS   Claim 4; Fig 11ak-al; 134pp; English.
XX
CC   This sequence is a truncated human telomerase of the invention. Primers
CC   that amplify the telomerase coding sequence can be used in a method for
CC   diagnosing cancer in a patient. The telomerase can be used for detection,
CC   diagnosis and drug screening. Inhibitors of telomerase activity can be
CC   used to treat cancers such as melanomas, other skin cancers,
CC   neuroblastomas, breast carcinomas, colon carcinomas, leukaemias,
CC   lymphomas, osteosarcomas or smooth muscle cell hyperplasias or skin
CC   growths. Enhancers of telomerase may be used to stimulate stem cell
CC   proliferation and differentiation (expansion of haematopoietic stem cells
CC   could be administered in the bone marrow transplant context). As well,
CC   many tissues have stem cells. Proliferation of these cells may be useful
CC   in wound healing, hair growth, treatment of disease such as Wilm's
CC   tumour, organ regeneration or differentiation after injury or diseases,
CC   nerve cell or brain cell growth following injury. Note: The N-terminus of
CC   this sequence can be replaced by the sequences shown in AAY00656-Y00658
XX
SQ   Sequence 936 AA;

  Query Match             82.6%;  Score 4923;  DB 2;  Length 936;
  Best Local Similarity   98.6%;  Pred. No. 0;
  Matches  934;  Conservative    0;  Mismatches    1;  Indels   12;  Gaps    1;

Qy          1 MPRAPRCRAVRSLLRSHYREVLPLATFVRRLGPQGWRLVQRGDPAAFRALVAQCLVCVPW 60
              |||||||||||||||| ||||||||||||||||||||||||||||||||||||||||||||
Db          1 MPRAPRCRAVRSLLRSHTREVLPLATFVRRLGPQGWRLVQRGDPAAFRALVAQCLVCVPW 60

Qy         61 DARPPPAAPSFRQVSCLKELVARVLQRLCERGAKNVLAFGFALLDGARGGPPEAFTTSVR 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 DARPPPAAPSFRQVSCLKELVARVLQRLCERGAKNVLAFGFALLDGARGGPPEAFTTSVR 120

Qy        121 SYLPNTVTDALRGSGAWGLLLRRVGDDVLVHLLARCALFVLVAPSCAYQVCGPPLYQLGA 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 SYLPNTVTDALRGSGAWGLLLRRVGDDVLVHLLARCALFVLVAPSCAYQVCGPPLYQLGA 180

Qy        181 ATQARPPPHASGPRRRLGCERAWNHSVREAGVPLGLPAPGARRRGGSASRSLPLPKRPRR 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 ATQARPPPHASGPRRRLGCERAWNHSVREAGVPLGLPAPGARRRGGSASRSLPLPKRPRR 240

Qy        241 GAAPEPERTPVGQGSWAHPGRTRGPSDRGFCVVSPARPAEEATSLEGALSGTRHSHPSVG 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 GAAPEPERTPVGQGSWAHPGRTRGPSDRGFCVVSPARPAEEATSLEGALSGTRHSHPSVG 300

Qy        301 RQHHAGPPSTSRPPRPWDTPCPPVYAETKHFLYSSGDKEQLRPSFLLSSLRPSLTGARRL 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 RQHHAGPPSTSRPPRPWDTPCPPVYAETKHFLYSSGDKEQLRPSFLLSSLRPSLTGARRL 360
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Qy        361 VETIFLGSRPWMPGTPRRLPRLPQRYWQMRPLFLELLGNHAQCPYGVLLKTHCPLRAAVT 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        361 VETIFLGSRPWMPGTPRRLPRLPQRYWQMRPLFLELLGNHAQCPYGVLLKTHCPLRAAVT 420

Qy        421 PAAGVCAREKPQGSVAAPEEEDTDPRRLVQLLRQHSSPWQVYGFVRACLRRLVPPGLWGS 480
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        421 PAAGVCAREKPQGSVAAPEEEDTDPRRLVQLLRQHSSPWQVYGFVRACLRRLVPPGLWGS 480

Qy        481 RHNERRFLRNTKKFISLGKHAKLSLQELTWKMSVRDCAWLRRSPGVGCVPAAEHRLREEI 540
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        481 RHNERRFLRNTKKFISLGKHAKLSLQELTWKMSVRDCAWLRRSPGVGCVPAAEHRLREEI 540

Qy        541 LAKFLHWLMSVYVVELLRSFFYVTETTFQKNRLFFYRKSVWSKLQSIGIRQHLKRVQLRE 600
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        541 LAKFLHWLMSVYVVELLRSFFYVTETTFQKNRLFFYRKSVWSKLQSIGIRQHLKRVQLRE 600

Qy        601 LSEAEVRQHREARPALLTSRLRFIPKPDGLRPIVNMDYVVGARTFRREKRAERLTSRVKA 660
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        601 LSEAEVRQHREARPALLTSRLRFIPKPDGLRPIVNMDYVVGARTFRREKRAERLTSRVKA 660

Qy        661 LFSVLNYERARRPGLLGASVLGLDDIHRAWRTFVLRVRAQDPPPELYFVKVDVTGAYDTI 720
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        661 LFSVLNYERARRPGLLGASVLGLDDIHRAWRTFVLRVRAQDPPPELYFVK---------- 710

Qy        721 PQDRLTEVIASIIKPQNTYCVRRYAVVQKAAHGHVRKAFKSHVSTLTDLQPYMRQFVAHL 780
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        711 --DRLTEVIASIIKPQNTYCVRRYAVVQKAAHGHVRKAFKSHVSTLTDLQPYMRQFVAHL 768

Qy        781 QETSPLRDAVVIEQSSSLNEASSGLFDVFLRFMCHHAVRIRGKSYVQCQGIPQGSILSTL 840
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        769 QETSPLRDAVVIEQSSSLNEASSGLFDVFLRFMCHHAVRIRGKSYVQCQGIPQGSILSTL 828

Qy        841 LCSLCYGDMENKLFAGIRRDGLLLRLVDDFLLVTPHLTHAKTFLRTLVRGVPEYGCVVNL 900
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        829 LCSLCYGDMENKLFAGIRRDGLLLRLVDDFLLVTPHLTHAKTFLRTLVRGVPEYGCVVNL 888

Qy        901 RKTVVNFPVEDEALGGTAFVQMPAHGLFPWCGLLLDTRTLEVQSDYS 947
              ||||||||||||||||||||||||||||||||||||||||||||||||
Db        889 RKTVVNFPVEDEALGGTAFVQMPAHGLFPWCGLLLDTRTLEVQSDYS 935
```

```
RESULT 47
AAW61349
ID   AAW61349 standard; protein; 949 AA.
XX
AC   AAW61349;
XX
DT   25-MAR-2003  (revised)
DT   12-OCT-1998  (first entry)
XX
DE   Human telomerase protein 2 (TP2) partial polypeptide.
XX
KW   TP2; human; telomerase protein 2; cancer; AIDS; ageing; therapy.
XX
OS   Homo sapiens.
XX
FH   Key             Location/Qualifiers
FT   Protein         1. .640
FT                   /note= "Claim 24"
FT   Protein         1. .563
FT                   /note= "Claim 24"
FT   Region          582. .587
FT   Protein         640. .940
FT                   /note= "Claim 22"
FT   Region          644. .648
FT   Protein         696. .953
FT                   /note= "Claim 24"
FT   Protein         696. .940
FT                   /note= "Claim 24"
FT   Region          852. .857
FT   Region          884. .8894
XX
PN   WO9821343-A1.
XX
PD   22-MAY-1998.
XX
PF   13-NOV-1997;   97WO-US021248.
XX
PR   15-NOV-1996;   96US-00751189.
PR   11-JUN-1997;   97US-00873039.
PR   16-OCT-1997;   97US-00951733.
XX
PA   (AMGE-) AMGEN INC.
PA   (AMGE-) AMGEN CANADA INC.
XX
PI   Harrington LA,  Robinson MO;
XX
DR   WPI; 1998-297946/26.
DR   N-PSDB; AAV27872.
XX
PT   New nucleic acid encoding human telomerase protein-2 - used for
PT   regulating telomerase activity, e.g. for treating cancer or acquired
PT   immune deficiency syndrome.
XX
PS   Claim 1d; Fig 6; 150pp; English.
XX
CC   This polypeptide comprises a large portion of human telomerase protein 2
CC   (TP2), a novel protein of the telomerase complex. Its amino acid sequence
CC   was deduced from partial cDNA clone 32 (see AAV27872), obtained from a
CC   human colon tumour cell line LIM1863 cDNA. A full-length polypeptide
CC   sequence (see AAW61350) is also disclosed. Expressing TP2 in a cell is
CC   used to increase telomerase activity and thus proliferation for treatment
CC   of e.g. HIV infection, AIDS and ageing disorders, while expressing an
CC   inactive mutant of TP2 (or molecule antisense to the gene) is used to
CC   decrease telomerase activity, e.g. for treatment of cancer. TR2
CC   polypeptides can also be used to screen for agents that inhibit TP2
CC   activity or its binding to TRIP1 (see AAW61347) or telomerase RNA,
CC   potentially useful therapeutically, also to raise specific antibodies
CC   useful in immunoassays and therapeutically as inhibitors. Also
CC   contemplated are transgenic animals in which the TP2 gene has been
CC   inactivated or is overexpressed. TP2 polypeptides are administered i.v.,
CC   s.c. or orally, or they are delivered from engineered cells or gene
CC   therapy vectors. (Updated on 25-MAR-2003 to correct PR field.)
XX
SQ   Sequence 949 AA;
```

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  Query Match             82.2%;  Score 4900;  DB 2;  Length 949;
  Best Local Similarity   100.0%;  Pred. No. 0;
  Matches  927;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 MPRAPRCRAVRSLLRSHYREVLPLATFVRRLGPQGWRLVQRGDPAAFRALVAQCLVCVPW 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         23 MPRAPRCRAVRSLLRSHYREVLPLATFVRRLGPQGWRLVQRGDPAAFRALVAQCLVCVPW 82

Qy         61 DARPPPAAPSFRQVSCLKELVARVLQRLCERGAKNVLAFGFALLDGARGGPPEAFTTSVR 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         83 DARPPPAAPSFRQVSCLKELVARVLQRLCERGAKNVLAFGFALLDGARGGPPEAFTTSVR 142

Qy        121 SYLPNTVTDALRGSGAWGLLLRRVGDDVLVHLLARCALFVLVAPSCAYQVCGPPLYQLGA 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        143 SYLPNTVTDALRGSGAWGLLLRRVGDDVLVHLLARCALFVLVAPSCAYQVCGPPLYQLGA 202

Qy        181 ATQARPPPHASGPRRRLGCERAWNHSVREAGVPLGLPAPGARRRGGSASRSLPLPKRPRR 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        203 ATQARPPPHASGPRRRLGCERAWNHSVREAGVPLGLPAPGARRRGGSASRSLPLPKRPRR 262

Qy        241 GAAPEPERTPVGQGSWAHPGRTRGPSDRGFCVVSPARPAEEATSLEGALSGTRHSHPSVG 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        263 GAAPEPERTPVGQGSWAHPGRTRGPSDRGFCVVSPARPAEEATSLEGALSGTRHSHPSVG 322

Qy        301 RQHHAGPPSTSRPPRPWDTPCPPVYAETKHFLYSSGDKEQLRPSFLLSSLRPSLTGARRL 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        323 RQHHAGPPSTSRPPRPWDTPCPPVYAETKHFLYSSGDKEQLRPSFLLSSLRPSLTGARRL 382

Qy        361 VETIFLGSRPWMPGTPRRLPRLPQRYWQMRPLFLELLGNHAQCPYGVLLKTHCPLRAAVT 420
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              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        383 VETIFLGSRPWMPGTPRRLPRLPQRYWQMRPLFLELLGNHAQCPYGVLLKTHCPLRAAVT 442

Qy        421 PAAGVCAREKPQGSVAAPEEEDTDPRRLVQLLRQHSSPWQVYGFVRACLRRLVPPGLWGS 480
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        443 PAAGVCAREKPQGSVAAPEEEDTDPRRLVQLLRQHSSPWQVYGFVRACLRRLVPPGLWGS 502

Qy        481 RHNERRFLRNTKKFISLGKHAKLSLQELTWKMSVRDCAWLRRSPGVGCVPAAEHRLREEI 540
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        503 RHNERRFLRNTKKFISLGKHAKLSLQELTWKMSVRDCAWLRRSPGVGCVPAAEHRLREEI 562

Qy        541 LAKFLHWLMSVYVVELLRSFFYVTETTFQKNRLFFYRKSVWSKLQSIGIRQHLKRVQLRE 600
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        563 LAKFLHWLMSVYVVELLRSFFYVTETTFQKNRLFFYRKSVWSKLQSIGIRQHLKRVQLRE 622

Qy        601 LSEAEVRQHREARPALLTSRLRFIPKPDGLRPIVNMDYVVGARTFRREKRAERLTSRVKA 660
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        623 LSEAEVRQHREARPALLTSRLRFIPKPDGLRPIVNMDYVVGARTFRREKRAERLTSRVKA 682

Qy        661 LFSVLNYERARRPGLLGASVLGLDDIHRAWRTFVLRVRAQDPPPELYFVKVDVTGAYDTI 720
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        683 LFSVLNYERARRPGLLGASVLGLDDIHRAWRTFVLRVRAQDPPPELYFVKVDVTGAYDTI 742

Qy        721 PQDRLTEVIASIIKPQNTYCVRRYAVVQKAAHGHVRKAFKSHVSTLTDLQPYMRQFVAHL 780
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        743 PQDRLTEVIASIIKPQNTYCVRRYAVVQKAAHGHVRKAFKSHVSTLTDLQPYMRQFVAHL 802

Qy        781 QETSPLRDAVVIEQSSSLNEASSGLFDVFLRFMCHHAVRIRGKSYVQCQGIPQGSILSTL 840
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        803 QETSPLRDAVVIEQSSSLNEASSGLFDVFLRFMCHHAVRIRGKSYVQCQGIPQGSILSTL 862

Qy        841 LCSLCYGDMENKLFAGIRRDGLLLRLVDDFLLVTPHLTHAKTFLRTLVRGVPEYGCVVNL 900
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        863 LCSLCYGDMENKLFAGIRRDGLLLRLVDDFLLVTPHLTHAKTFLRTLVRGVPEYGCVVNL 922

Qy        901 RKTVVNFPVEDEALGGTAFVQMPAHGL 927
              |||||||||||||||||||||||||||
Db        923 RKTVVNFPVEDEALGGTAFVQMPAHGL 949
```

RESULT 48
ADG90609
ID   ADG90609 standard; protein; 1152 AA.
XX
AC   ADG90609;
XX
DT   25-MAR-2004 (first entry)
XX
DE   TERT consensus sequence SEQ ID NO:12.
XX
KW   immune response; telomerase reverse transcriptase; TERT; cytostatic;
KW   immunostimulant; cancer; cytotoxic T cell response.
XX
OS   Unidentified.
XX
PN   WO2004002408-A2.
XX
PD   08-JAN-2004.
XX
PF   24-JUN-2003; 2003WO-US019844.
XX
PR   27-JUN-2002; 2002US-0393295P.
XX
PA   (GERO-) GERON CORP.
XX
PI   Majumdar A, Ferber IA, Frolkis M, Wang Z;
XX
DR   WPI; 2004-071946/07.
XX
PT   Eliciting an immune response in a mammal specific for its own telomerase
PT   reverse transcriptase (TERT), useful for treating or preventing cancer,
PT   comprises administering a composition containing TERT of another
PT   mammalian species.
XX
PS   Claim 10; SEQ ID NO 12; 44pp; English.
XX
CC   The invention relates to a novel method for eliciting an immune response
CC   in a mammalian subject that is specific for its own telomerase reverse
CC   transcriptase (TERT), comprising administering an immunogenic composition
CC   containing a protein with at least 20 consecutive amino acids of TERT of
CC   another mammalian species, or a nucleic acid encoding the protein. A
CC   composition of the invention has cytostatic, and immunostimulant
CC   activity. The protein or the nucleic acid encoding the protein is useful
CC   in the manufacture of a medicament for the treatment of cancer in a human
CC   or for eliciting a cytotoxic T cell response in a human.
XX
SQ   Sequence 1152 AA;

```
  Query Match             75.7%;  Score 4515;  DB 8;  Length 1152;
  Best Local Similarity   76.4%;  Pred. No. 0;
  Matches  880;  Conservative   87;  Mismatches  165;  Indels   20;  Gaps    6;

Qy          1 MPRAPRCRAVRSLLRSHYREVLPLATFVRRLGPQGWRLVQRGDPAAFRALVAQCLVCVPW 60
              |||||||||||:|||||||||||||||||||||:| |||| |||||||||||||||||||
Db          1 MPRAPRCRAVRALLRSHYREVLPLATFVRRLGPEGRRLVQPGDPAAFRALVAQCLVCVPW 60

Qy         61 DARPPPAAPSFRQVSCLKELVARVLQRLCERGAKNVLAFGFALLDGARGGPPEAFTTSVR 120
               |||||||||| ||| ||||||||:||||||| :|||||||||||||||||| |||||||
Db         61 GARPPPAAPSFHQVSSLKELVARVVQRLCERGERNVLAFGFALLDGARGGPPMAFTTSVR 120

Qy        121 SYLPNTVTDALRGSGAWGLLLRRVGDDVLVHLLARCALFVLVAPSCAYQVCGPPLYQLGA 180
              ||||||||: |||||||||||||||||:||||||||||::|||||||||||||||||:||
Db        121 SYLPNTVTETLRGSGAWGLLLRRVGDDLLVHLLARCALYLLVAPSCAYQVCGPPLYQIGA 180

Qy        181 ATQARPPPHASG-PRRRLG--------CERAWNHSVREAGVPLGLPAPGARRRGGSASRS 231
               ||||||||||| ||| :|        |||||||||||||||||||:|||:|||||||||
Db        181 TTQARPPPHASGRPRRPVGRNFTNLGFCERAWNHSVREAGVPLGLPSPGAKRRGGSASRS 240

Qy        232 LPLPKRPRRGAAPEPERTPVGQGSWAHPGRTRGPSDRGFCVVSPARPAEEATSLEGALSG 291
              |||||: ||||||||||||||||||   |||| ||| |  ||||||||||  | :| :| 
Db        241 LPLPKKARRGAAPEPERTPVGQGSWTPSGRTRVPSDAGSPVVSPARPAEEDLSSKGKVSD 300

Qy        292 TRHSHPSVGRQHHAGPPSTSRPPRPWDTPCPPVYAETKHFLYSSGDKEQLRPSFLLSSLR 351
                 |     :   : ||| | ||||      |||||||||||||| :|:||||||||:|:
Db        301 LSLSGSVCCKHKPSSPPSLSSPPRPNAFQLRPVYAETKHFLYSSGGRERLRPSFLLSNLQ 360

Qy        352 PSLTGARRLVETIFLGSRPWMPGTPRRLPRLPQRYWQMRPLFLELLGNHAQCPYGVLLKT 411
              ||||||||||||||||||||  |   |  || :||||||||| |||||||:|||  ||::
Db        361 PSLTGARRLVETIFLGSRPWTSGPLCRTHRLSRRYWQMRPLFQELLGNHARCPYVRLLRS 420

Qy        412 HCPLRAAVTPAAGVCAREKPQGSVAAPEE-----EDTDPRRLVQLLRQHSSPWQVYGFVR 466
              ||||||| || ||      ||||||||||     | ||  ||:|||||||||||||||:|
Db        421 HCPLRAAATPVAGALNTSPPQGSVAAPEEVAAPQEQTDSTRLMQLLRQHSSPWQVYGFLR 480

Qy        467 ACLRRLVPPGLWGSRHNERRFLRNTKKFISLGKHAKLSLQELTWKMSVRDCAWLRRSPGV 526
              ||| :|||||||||||||||||:| ||||||||||||||||||||| |||||||| ||| 
Db        481 ACLCKLVPPGLWGSRHNERRFLKNVKKFISLGKHAKLSLQELTWKMKVRDCAWLRSSPGY 540

Qy        527 GCVPAAEHRLREEILAK---FLHWLMSVYVVELLRSFFYVTETTFQKNRLFFYRKSVWSK 583
                |||||||||| ||||   || ||||||||||||||||:||:|||||||||||||||||
Db        541 ESVPAAEHRLRERILAKEHPFLFWLMSVYVVELLRSFFYITESTFQKNRLFFYRKSVWSK 600

Qy        584 LQSIGIRQHLKRVQLRELSEAEVRQHREARPALLTSRLRFIPKPDGLRPIVNMDYVVGAR 643
              |||||:||||:||:|||||: |||||:|| || :   ||||||||:|||||||| | :| |
Db        601 LQSIGVRQHLERVRLRELSQEEVRQHQEAWPAMPICRLRFIPKPNGLRPIVNMSYSMGTR 660

Qy        644 TFRREKRAERLTSRVKALFSVLNYERARRPGLLGASVLGLDDIHRAWRTFVLRVRAQDPP 703
               | | |:|:  | |:| ||||||||| : | ||||||||::||:| |||||||||| || 
Db        661 AFGRRKQAQHFTQRLKTLFSVLNYERTKHPHLLGASVLGMNDIYRTWRTFVLRVRALDPT 720

Qy        704 PELYFVKVDVTGAYDTIPQDRLTEVIASIIK-PQNTYCVRRYAVVQKAAHGHVRKAFKSH 762
              | :|||| ||||||| ||||:| ||||::|:  ::|||:|:|||||: | | | |:|:  
Db        721 PRMYFVKADVTGAYDAIPQDKLVEVIANMIRHSESTYCIRQYAVVQRDAQGQVHKSFRRQ 780

Qy        763 VSTLTDLQPYMRQFVAHLQET--SPLRDAVVIEQSSSLNEASSGLFDVFLRFMCHHAVRI 820
              ||||:||||||| ||: |||::  | ||::||||||| ||||||| ||| ||||: |   |:|
```

```
Db        781 VSTLSDLQPYMGQFLKHLQDSDASALRNSVVIEQSISLNEASSSLFDFFLRFLRHSVVKI 840

Qy        821 RGKSYVQCQGIPQGSILSTLLCSLCYGDMENKLFAGIRRDGLLLRLVDDFLLVTPHLTHA 880
              |: |||||||||||| |||||||||:||||||||| ::||||||| ||||||||||  |
Db        841 GGRCYVQCQGIPQGSSLSTLLCSLCFGDMENKLFAEVQRDGLLLRFVDDFLLVTPHLDQA 900

Qy        881 KTFLRTLVRGVPEYGCVVNLRKTVVNFPVEDEALGGTAFVQMPAHGLFPWCGLLLDTRTL 940
              |||| ||||||||||::||:|||||||||    |||||  |:||| ||||||||||:||
Db        901 KTFLSTLVRGVPEYGCMINLQKTVVNFPVEPGTLGGTAPYQLPAHCLFPWCGLLLDTQTL 960

Qy        941 EVQSDYSSYARTSIRASLTFNRGFKAGRNMRRKLFGVLRLKCHSLFLDLQVNSLQTVCTN 1000
              ||  ||| ||||||:||||| | ||||:||| ||  ||||||||||||||||||||| |
Db        961 EVFCDYSGYARTSIKASLTFQRVFKAGKNMRNKLLSVLRLKCHSLFLDLQVNSLQTVCIN 1020

Qy       1001 IYKILLLQAYRFHACVLQLPFHQQVWKNPTFFLRVISDTASLCYSILKAKNAGMSLGAKG 1060
              |||| ||||||||||:|||| |:| ||||||| :||  || ||:||| |||||:| |||
Db       1021 IYKIFLLQAYRFHACVIQLPFDQRVRKNPTFFLGIISSQASCCYAILKVKNAGMTLKAKG 1080

Qy       1061 AAGPLPSEAVQWLCHQAFLLKLTRHRVTYVPLLGSLRTAQTQLSRKLPGTTLTALEAAAN 1120
              |||  | ||  |||:|||||||  | |||  ||| ||||| || ||||  |:| |||||:
Db       1081 AAGSFPPEAAHWLCYQAFLLKLAAHSVTYKCLLGPLRTAQKQLCRKLPEATMTILEAAAD 1140

Qy       1121 PALPSDFKTILD 1132
              ||| :||:||||
Db       1141 PALSTDFQTILD 1152
```

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RESULT 49
AAW46997
ID   AAW46997 standard; protein; 807 AA.
XX
AC   AAW46997;
XX
DT   13-AUG-1998  (first entry)
XX
DE   Human telomerase reverse transcriptase Delta182 variant.
XX
KW   Human; telomerase reverse transcriptase; hTRT; TRT; diagnosis; prognosis;
KW   cell proliferation; cancer; ageing; ribonucleoprotein.
XX
OS   Synthetic.
OS   Homo sapiens.
XX
PN   GB2317891-A.
XX
PD   08-APR-1998.
XX
PF   01-OCT-1997;   97GB-00020890.
XX
PR   01-OCT-1996;   96US-00724643.
PR   18-APR-1997;   97US-00844419.
PR   25-APR-1997;   97US-00846017.
PR   06-MAY-1997;   97US-00851843.
PR   09-MAY-1997;   97US-00854050.
PR   14-AUG-1997;   97US-00911312.
PR   14-AUG-1997;   97US-00912951.
PR   14-AUG-1997;   97US-00915503.
XX
PA   (GERO-) GERON CORP.
PA   (UYTE-) UNIV TECHNOLOGY CORP.
XX
PI   Cech TR,  Lingner J,  Nakamura T,  Chapman KB,  Morin GB,  Harley CB;
PI   Andrews WH;
XX
DR   WPI; 1998-171633/16.
DR   N-PSDB; AAV22382.
XX
PT   Pure and recombinant human Telomerase Reverse Transcriptase and its
PT   variants - are useful in the diagnosis, prognosis and treatment of cell
PT   proliferation conditions especially cancer and ageing.
XX
PS   Disclosure; Fig 20; 387pp; English.
XX
CC   The present sequence represents a human telomerase reverse transcriptase
CC   (hTRT) variant from the present invention. The present invention also
CC   describes the following methods: (A) determining whether a test compound
CC   is a modulator of hTRT, by detecting the change in hTRT recombinant
CC   protein or polynucleotide, on administration of the compound; (B)
CC   preparation of recombinant telomerase by contacting a protein preparation
CC   of hTRT with a telomerase RNA component; (C) detection of the hTRT RNA or
CC   protein in a sample by binding a relevant probe to the sample and
CC   detecting the complex formed or in the case of RNA detection, amplifying
CC   the product and correlating the presence of complex or amplification
CC   product with presence of hTRT in the sample; and (D) increasing the
CC   proliferation of a vertebrate cell by increasing hTRT expression; and (E)
CC   the use of an agent that causes an increase in cell vertebrate cell
CC   proliferation to create a medicament that inhibits ageing. A protein
CC   preparation of hTRT and the polynucleotide encoding hTRT can be used in
CC   the manufacture of medicaments for inhibiting the effect of ageing or
CC   cancer. Inhibitors of telomerase activity can be used to treat conditions
CC   that are associated with high telomerase activity. A protein preparation
CC   of hTRT can also be used in the new methods
XX
SQ   Sequence 807 AA;
```

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  Query Match             68.0%;  Score 4052;  DB 2;  Length 807;
  Best Local Similarity   100.0%;  Pred. No. 0;
  Matches  763;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 MPRAPRCRAVRSLLRSHYREVLPLATFVRRLGPQGWRLVQRGDPAAFRALVAQCLVCVPW 60
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 MPRAPRCRAVRSLLRSHYREVLPLATFVRRLGPQGWRLVQRGDPAAFRALVAQCLVCVPW 60

Qy         61 DARPPPAAPSFRQVSCLKELVARVLQRLCERGAKNVLAFGFALLDGARGGPPEAFTTSVR 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 DARPPPAAPSFRQVSCLKELVARVLQRLCERGAKNVLAFGFALLDGARGGPPEAFTTSVR 120

Qy        121 SYLPNTVTDALRGSGAWGLLLRRVGDDVLVHLLARCALFVLVAPSCAYQVCGPPLYQLGA 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 SYLPNTVTDALRGSGAWGLLLRRVGDDVLVHLLARCALFVLVAPSCAYQVCGPPLYQLGA 180

Qy        181 ATQARPPPHASGPRRRLGCERAWNHSVREAGVPLGLPAPGARRRGGSASRSLPLPKRPRR 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 ATQARPPPHASGPRRRLGCERAWNHSVREAGVPLGLPAPGARRRGGSASRSLPLPKRPRR 240

Qy        241 GAAPEPERTPVGQGSWAHPGRTRGPSDRGFCVVSPARPAEEATSLEGALSGTRHSHPSVG 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 GAAPEPERTPVGQGSWAHPGRTRGPSDRGFCVVSPARPAEEATSLEGALSGTRHSHPSVG 300

Qy        301 RQHHAGPPSTSRPPRPWDTPCPPVYAETKHFLYSSGDKEQLRPSFLLSSLRPSLTGARRL 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 RQHHAGPPSTSRPPRPWDTPCPPVYAETKHFLYSSGDKEQLRPSFLLSSLRPSLTGARRL 360

Qy        361 VETIFLGSRPWMPGTPRRLPRLPQRYWQMRPLFLELLGNHAQCPYGVLLKTHCPLRAAVT 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        361 VETIFLGSRPWMPGTPRRLPRLPQRYWQMRPLFLELLGNHAQCPYGVLLKTHCPLRAAVT 420

Qy        421 PAAGVCAREKPQGSVAAPEEEDTDPRRLVQLLRQHSSPWQVYGFVRACLRRLVPPGLWGS 480
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        421 PAAGVCAREKPQGSVAAPEEEDTDPRRLVQLLRQHSSPWQVYGFVRACLRRLVPPGLWGS 480

Qy        481 RHNERRFLRNTKKFISLGKHAKLSLQELTWKMSVRDCAWLRRSPGVGCVPAAEHRLREEI 540
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        481 RHNERRFLRNTKKFISLGKHAKLSLQELTWKMSVRDCAWLRRSPGVGCVPAAEHRLREEI 540

Qy        541 LAKFLHWLMSVYVVELLRSFFYVTETTFQKNRLFFYRKSVWSKLQSIGIRQHLKRVQLRE 600
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        541 LAKFLHWLMSVYVVELLRSFFYVTETTFQKNRLFFYRKSVWSKLQSIGIRQHLKRVQLRE 600

Qy        601 LSEAEVRQHREARPALLTSRLRFIPKPDGLRPIVNMDYVVGARTFRREKRAERLTSRVKA 660
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        601 LSEAEVRQHREARPALLTSRLRFIPKPDGLRPIVNMDYVVGARTFRREKRAERLTSRVKA 660

Qy        661 LFSVLNYERARRPGLLGASVLGLDDIHRAWRTFVLRVRAQDPPPELYFVKVDVTGAYDTI 720
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        661 LFSVLNYERARRPGLLGASVLGLDDIHRAWRTFVLRVRAQDPPPELYFVKVDVTGAYDTI 720
```

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Qy        721 PQDRLTEVIASIIKPQNTYCVRRYAVVQKAAHGHVRKAFKSHV 763
              |||||||||||||||||||||||||||||||||||||||||||||
Db        721 PQDRLTEVIASIIKPQNTYCVRRYAVVQKAAHGHVRKAFKSHV 763


RESULT 50
AAY00637
ID   AAY00637 standard; protein; 807 AA.
XX
AC   AAY00637;
XX
DT   26-JUL-1999  (first entry)
XX
DE   N-terminal truncated telomerase protein sequence.
XX
KW   Telomerase; human; cancer; diagnosis; melanoma; skin cancer; leukaemia;
KW   neuroblastoma; breast carcinoma; colon carcinoma; lymphoma; osteosarcoma;
KW   smooth muscle cell hyperplasia; stem cell proliferation; Wilm's tumour;
KW   stem cell differentiation; organ regeneration; organ differentiation.
XX
OS   Homo sapiens.
OS   Synthetic.
XX
PN   WO9901560-A1.
XX
PD   14-JAN-1999.
XX
PF   01-JUL-1998;   98WO-US013835.
XX
PR   01-JUL-1997;   97US-0051410P.
PR   21-JUL-1997;   97US-0053018P.
PR   21-JUL-1997;   97US-0053329P.
PR   04-AUG-1997;   97US-0054642P.
PR   09-SEP-1997;   97US-0058287P.
XX
PA   (CAMB-) CAMBIA BIOSYSTEMS LLC.
XX
PI   Kilian A,  Bowtell D;
XX
DR   WPI; 1999-106060/09.
DR   N-PSDB; AAX18265.
XX
PT   New isolated vertebrate telomerase genes - used to develop products for
PT   treating cancers or for organ regeneration, nerve cell or brain cell
PT   growth following injury or bone marrow transplantation.
XX
PS   Claim 4; Fig 11d-e; 134pp; English.
XX
CC   This sequence is a truncated human telomerase of the invention. Primers
CC   that amplify the telomerase coding sequence can be used in a method for
CC   diagnosing cancer in a patient. The telomerase can be used for detection,
CC   diagnosis and drug screening. Inhibitors of telomerase activity can be
CC   used to treat cancers such as melanomas, other skin cancers,
CC   neuroblastomas, breast carcinomas, colon carcinomas, leukaemias,
CC   lymphomas, osteosarcomas or smooth muscle cell hyperplasias or skin
CC   growths. Enhancers of telomerase may be used to stimulate stem cell
CC   proliferation and differentiation (expansion of haematopoietic stem cells
CC   could be administered in the bone marrow transplant context). As well,
CC   many tissues have stem cells. Proliferation of these cells may be useful
CC   in wound healing, hair growth, treatment of disease such as Wilm's
CC   tumour, organ regeneration or differentiation after injury or diseases,
CC   nerve cell or brain cell growth following injury
XX
SQ   Sequence 807 AA;

  Query Match             68.0%;  Score 4052;  DB 2;  Length 807;
  Best Local Similarity   100.0%;  Pred. No. 0;
  Matches  763;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 MPRAPRCRAVRSLLRSHYREVLPLATFVRRLGPQGWRLVQRGDPAAFRALVAQCLVCVPW 60
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 MPRAPRCRAVRSLLRSHYREVLPLATFVRRLGPQGWRLVQRGDPAAFRALVAQCLVCVPW 60

Qy         61 DARPPPAAPSFRQVSCLKELVARVLQRLCERGAKNVLAFGFALLDGARGGPPEAFTTSVR 120
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 DARPPPAAPSFRQVSCLKELVARVLQRLCERGAKNVLAFGFALLDGARGGPPEAFTTSVR 120

Qy        121 SYLPNTVTDALRGSGAWGLLLRRVGDDVLVHLLARCALFVLVAPSCAYQVCGPPLYQLGA 180
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 SYLPNTVTDALRGSGAWGLLLRRVGDDVLVHLLARCALFVLVAPSCAYQVCGPPLYQLGA 180

Qy        181 ATQARPPPHASGPRRRLGCERAWNHSVREAGVPLGLPAPGARRRGGSASRSLPLPKRPRR 240
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 ATQARPPPHASGPRRRLGCERAWNHSVREAGVPLGLPAPGARRRGGSASRSLPLPKRPRR 240

Qy        241 GAAPEPERTPVGQGSWAHPGRTRGPSDRGFCVVSPARPAEEATSLEGALSGTRHSHPSVG 300
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 GAAPEPERTPVGQGSWAHPGRTRGPSDRGFCVVSPARPAEEATSLEGALSGTRHSHPSVG 300

Qy        301 RQHHAGPPSTSRPPRPWDTPCPPVYAETKHFLYSSGDKEQLRPSFLLSSLRPSLTGARRL 360
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 RQHHAGPPSTSRPPRPWDTPCPPVYAETKHFLYSSGDKEQLRPSFLLSSLRPSLTGARRL 360

Qy        361 VETIFLGSRPWMPGTPRRLPRLPQRYWQMRPLFLELLGNHAQCPYGVLLKTHCPLRAAVT 420
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        361 VETIFLGSRPWMPGTPRRLPRLPQRYWQMRPLFLELLGNHAQCPYGVLLKTHCPLRAAVT 420

Qy        421 PAAGVCAREKPQGSVAAPEEEDTDPRRLVQLLRQHSSPWQVYGFVRACLRRLVPPGLWGS 480
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        421 PAAGVCAREKPQGSVAAPEEEDTDPRRLVQLLRQHSSPWQVYGFVRACLRRLVPPGLWGS 480

Qy        481 RHNERRFLRNTKKFISLGKHAKLSLQELTWKMSVRDCAWLRRSPGVGCVPAAEHRLREEI 540
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        481 RHNERRFLRNTKKFISLGKHAKLSLQELTWKMSVRDCAWLRRSPGVGCVPAAEHRLREEI 540

Qy        541 LAKFLHWLMSVYVVELLRSFFYVTETTFQKNRLFFYRKSVWSKLQSIGIRQHLKRVQLRE 600
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        541 LAKFLHWLMSVYVVELLRSFFYVTETTFQKNRLFFYRKSVWSKLQSIGIRQHLKRVQLRE 600

Qy        601 LSEAEVRQHREARPALLTSRLRFIPKPDGLRPIVNMDYVVGARTFRREKRAERLTSRVKA 660
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        601 LSEAEVRQHREARPALLTSRLRFIPKPDGLRPIVNMDYVVGARTFRREKRAERLTSRVKA 660

Qy        661 LFSVLNYERARRPGLLGASVLGLDDIHRAWRTFVLRVRAQDPPPELYFVKVDVTGAYDTI 720
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        661 LFSVLNYERARRPGLLGASVLGLDDIHRAWRTFVLRVRAQDPPPELYFVKVDVTGAYDTI 720

Qy        721 PQDRLTEVIASIIKPQNTYCVRRYAVVQKAAHGHVRKAFKSHV 763
              |||||||||||||||||||||||||||||||||||||||||||||
Db        721 PQDRLTEVIASIIKPQNTYCVRRYAVVQKAAHGHVRKAFKSHV 763


RESULT 51
AAY00646
ID   AAY00646 standard; protein; 807 AA.
XX
AC   AAY00646;
XX
DT   26-JUL-1999  (first entry)
XX
DE   Truncated telomerase (ver. 2) protein sequence.
XX
KW   Telomerase; human; cancer; diagnosis; melanoma; skin cancer; leukaemia;
KW   neuroblastoma; breast carcinoma; colon carcinoma; lymphoma; osteosarcoma;
KW   smooth muscle cell hyperplasia; stem cell proliferation; Wilm's tumour;
KW   stem cell differentiation; organ regeneration; organ differentiation.
XX
OS   Homo sapiens.
OS   Synthetic.
XX
PN   WO9901560-A1.
XX
PD   14-JAN-1999.
XX
PF   01-JUL-1998;   98WO-US013835.
```

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XX
PR   01-JUL-1997;   97US-0051410P.
PR   21-JUL-1997;   97US-0053018P.
PR   21-JUL-1997;   97US-0053329P.
PR   04-AUG-1997;   97US-0054642P.
PR   09-SEP-1997;   97US-0058287P.
XX
PA   (CAMB-) CAMBIA BIOSYSTEMS LLC.
XX
PI   Kilian A,  Bowtell D;
XX
DR   WPI; 1999-106060/09.
DR   N-PSDB; AAX18274.
XX
PT   New isolated vertebrate telomerase genes - used to develop products for
PT   treating cancers or for organ regeneration, nerve cell or brain cell
PT   growth following injury or bone marrow transplantation.
XX
PS   Claim 4; Fig 11x-y; 134pp; English.
XX
CC   This sequence is a truncated human telomerase of the invention. Primers
CC   that amplify the telomerase coding sequence can be used in a method for
CC   diagnosing cancer in a patient. The telomerase can be used for detection,
CC   diagnosis and drug screening. Inhibitors of telomerase activity can be
CC   used to treat cancers such as melanomas, other skin cancers,
CC   neuroblastomas, breast carcinomas, colon carcinomas, leukaemias,
CC   lymphomas, osteosarcomas or smooth muscle cell hyperplasias or skin
CC   growths. Enhancers of telomerase may be used to stimulate stem cell
CC   proliferation and differentiation (expansion of haematopoietic stem cells
CC   could be administered in the bone marrow transplant context). As well,
CC   many tissues have stem cells. Proliferation of these cells may be useful
CC   in wound healing, hair growth, treatment of disease such as Wilm's
CC   tumour, organ regeneration or differentiation after injury or diseases,
CC   nerve cell or brain cell growth following injury. Note: The N-terminus of
CC   this sequence can be replaced by the sequences shown in AAY00656-Y00658
XX
SQ   Sequence 807 AA;

  Query Match             68.0%;  Score 4052;  DB 2;  Length 807;
  Best Local Similarity   100.0%;  Pred. No. 0;
  Matches  763;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 MPRAPRCRAVRSLLRSHYREVLPLATFVRRLGPQGWRLVQRGDPAAFRALVAQCLVCVPW 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 MPRAPRCRAVRSLLRSHYREVLPLATFVRRLGPQGWRLVQRGDPAAFRALVAQCLVCVPW 60

Qy         61 DARPPPAAPSFRQVSCLKELVARVLQRLCERGAKNVLAFGFALLDGARGGPPEAFTTSVR 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 DARPPPAAPSFRQVSCLKELVARVLQRLCERGAKNVLAFGFALLDGARGGPPEAFTTSVR 120

Qy        121 SYLPNTVTDALRGSGAWGLLLRRVGDDVLVHLLARCALFVLVAPSCAYQVCGPPLYQLGA 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 SYLPNTVTDALRGSGAWGLLLRRVGDDVLVHLLARCALFVLVAPSCAYQVCGPPLYQLGA 180

Qy        181 ATQARPPPHASGPRRRLGCERAWNHSVREAGVPLGLPAPGARRRGGSASRSLPLPKRPRR 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 ATQARPPPHASGPRRRLGCERAWNHSVREAGVPLGLPAPGARRRGGSASRSLPLPKRPRR 240

Qy        241 GAAPEPERTPVGQGSWAHPGRTRGPSDRGFCVVSPARPAEEATSLEGALSGTRHSHPSVG 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 GAAPEPERTPVGQGSWAHPGRTRGPSDRGFCVVSPARPAEEATSLEGALSGTRHSHPSVG 300

Qy        301 RQHHAGPPSTSRPPRPWDTPCPPVYAETKHFLYSSGDKEQLRPSFLLSSLRPSLTGARRL 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 RQHHAGPPSTSRPPRPWDTPCPPVYAETKHFLYSSGDKEQLRPSFLLSSLRPSLTGARRL 360

Qy        361 VETIFLGSRPWMPGTPRRLPRLPQRYWQMRPLFLELLGNHAQCPYGVLLKTHCPLRAAVT 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        361 VETIFLGSRPWMPGTPRRLPRLPQRYWQMRPLFLELLGNHAQCPYGVLLKTHCPLRAAVT 420

Qy        421 PAAGVCAREKPQGSVAAPEEEDTDPRRLVQLLRQHSSPWQVYGFVRACLRRLVPPGLWGS 480
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        421 PAAGVCAREKPQGSVAAPEEEDTDPRRLVQLLRQHSSPWQVYGFVRACLRRLVPPGLWGS 480

Qy        481 RHNERRFLRNTKKFISLGKHAKLSLQELTWKMSVRDCAWLRRSPGVGCVPAAEHRLREEI 540
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        481 RHNERRFLRNTKKFISLGKHAKLSLQELTWKMSVRDCAWLRRSPGVGCVPAAEHRLREEI 540

Qy        541 LAKFLHWLMSVYVVELLRSFFYVTETTFQKNRLFFYRKSVWSKLQSIGIRQHLKRVQLRE 600
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        541 LAKFLHWLMSVYVVELLRSFFYVTETTFQKNRLFFYRKSVWSKLQSIGIRQHLKRVQLRE 600

Qy        601 LSEAEVRQHREARPALLTSRLRFIPKPDGLRPIVNMDYVVGARTFRREKRAERLTSRVKA 660
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        601 LSEAEVRQHREARPALLTSRLRFIPKPDGLRPIVNMDYVVGARTFRREKRAERLTSRVKA 660

Qy        661 LFSVLNYERARRPGLLGASVLGLDDIHRAWRTFVLRVRAQDPPPELYFVKVDVTGAYDTI 720
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        661 LFSVLNYERARRPGLLGASVLGLDDIHRAWRTFVLRVRAQDPPPELYFVKVDVTGAYDTI 720

Qy        721 PQDRLTEVIASIIKPQNTYCVRRYAVVQKAAHGHVRKAFKSHV 763
              |||||||||||||||||||||||||||||||||||||||||||
Db        721 PQDRLTEVIASIIKPQNTYCVRRYAVVQKAAHGHVRKAFKSHV 763


RESULT 52
ADD21416
ID   ADD21416 standard; protein; 1128 AA.
XX
AC   ADD21416;
XX
DT   15-JAN-2004  (first entry)
XX
DE   Golden hamster TERT protein related to continual cell growth.
XX
KW   continual growth; cultured cell; cyclin dependent kinase; cdk4; cdk2;
KW   cdk6; activating mutation; cell growth; cell division; cell cycle;
KW   cancer-causing agent; continual growth-induced cell; enzyme; TERT;
KW   telomerase; Golden hamster.
XX
OS   Mesocricetus auratus.
XX
PN   WO2003044169-A2.
XX
PD   30-MAY-2003.
XX
PF   15-NOV-2002; 2002WO-US036729.
XX
PR   15-NOV-2001; 2001US-0334760P.
XX
PA   (UTEM ) UNIV TEMPLE.
XX
PI   Reddy PE,  Rane SG,  Mettus RV;
XX
DR   WPI; 2003-449813/42.
XX
PT   A composition for reversibly inducing continual growth in normal cells
PT   comprises a cyclin dependent kinase protein (e.g. cdk4, cdk2 or cdk6) or
PT   its active fragment, derivative, homolog or analog, having an activating
PT   mutation.
XX
PS   Disclosure; Page 119-121; 77pp; English.
XX
CC   This invention relates to a novel composition for inducing a reversible
CC   state of a continual growth in cultured cells and comprises at least one
CC   compound comprising a cyclin dependent kinase (cdk)4, cdk2 or cdk6
CC   protein having an activating mutation. Growth and division of living
CC   cells involve a regular series of events and processes that comprise the
CC   cell cycle. Cyclin dependent kinases cdk2, cdk4 and cdk6 are involved in
CC   the control of G1, the point at which cells irrevocably commit to DNA
CC   synthesis and thus enter the cell cycle. The invention is useful in
CC   reversibly inducing continual growth in normal cells and may allow the
CC   screening of cancer-causing agents with the continual growth-induced
CC   cells. The present sequence is that of the golden hamster TERT protein,
CC   the catalytic subunit of telomerase, related to the invention. Note: Due
CC   to an error in the specification or sequence listing, the Seq ID numbers
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CC   given in the disclosure do not correspond to those given in the sequence
CC   listing. It is therefore unclear which Seq ID number corresponds to which
CC   sequence and exactly which sequence is being claimed.
XX
SQ   Sequence 1128 AA;

  Query Match             60.9%;  Score 3628;  DB 7;  Length 1128;
  Best Local Similarity   63.3%;  Pred. No. 9.8e-296;
  Matches  736;  Conservative  124;  Mismatches  238;  Indels   64;  Gaps   16;

Qy          1 MPRAPRCRAVRSLLRSHYREVLPLATFVRRLGPQGWRLVQRGDPAAFRALVAQCLVCVPW 60
              ||||||||||||:|||| ||:| ||||||||||||:| :||| |||  || |||:|||||||
Db          1 MPRAPRCRAVRALLRSQYRQVWPLATFVRRLGPEGRQLVQPGDPKVFRTLVARCLVCVPW 60

Qy         61 DARPPPAAPSFRQVSCLKELVARVLQRLCERGAKNVLAFGFALLDGARGGPPEAFTTSVR 120
              |::||||  || ||| ||||||||:||||||| :||| ||||||:||:||||  ||||||
Db         61 DSQPPPADLSFHQVSSLKELVARVVQRLCERGERNVLTFGFALLNGAQGGPPMTFTTSVR 120

Qy        121 SYLPNTVTDALRGSGAWGLLLRRVGDDVLVHLLARCALFVLVAPSCAYQVCGPPLYQLGA 180
              |||||:||::|| |||| ||| |||||:||:|||||||::|| ||||||||| ||||: |
Db        121 SYLPNSVTESLRVSGAWMLLLNRVGDDLLVYLLARCALYLLVPPSCAYQVCGSPLYQICA 180

Qy        181 ATQARPP-PHASGPRRRLG--------CERAWNHSVREAGVPLGLPAPGARRRGGSASRS 231
                :  |       | | :|          |  | | :||  |  ||:  |:|     :||
Db        181 TAETWPSVSRIYRPTRPVGRNFTHLGSTHRVRNSSHQEAWKPPPLPSREAKRSLSITNRS 240

Qy        232 LPLPKRPRRGAAPEPERTPVGQGSWAHPGRTRGPSDRGFCVVSPAR----PAEEATSLEG 287
              :|  |: |   ||  |: |  |          |||: : | :||:    |    |  |
Db        241 VPPSKKARCDLAPRLEKGPYRQA-------VPTPSDKTW-VPNPAKSHAVPISRTTK-ED 291

Qy        288 ALSGTRHSHPSVGRQ----HHAGPPSTS-RPP--------RPWDTPCPPVYAETKHFLYS 334
                || :   | : |     :   | ||| : |         ||         | ||| ||||
Db        292 LSSGVK--APGLSRSGSVCYKHKPSSTSLQSPLCQNAFQLRP--------YTETKRFLYS 341

Qy        335 -SGDKEQLRPSFLLSSLRPSLTGARRLVETIFLGSRPWMPGTPRRLPRLPQRYWQMRPLF 393
               | :|:| |||||::|:||||||||||| :||| ||   |      || :|||||||||
Db        342 REGGRERLNPSFLLNNLQPSLTGARRLVEILFLGMRPRTSGPLCGRRRLSKRYWQMRPLF 401

Qy        394 LELLGNHAQCPYGVLLKTHCPLRAAVTPAAGVCAREKPQGSVAAPEEEDTDPRRLVQLLR 453
              :|| |||:|||  ||::||  | |    ||                | |:||: |||
Db        402 QQLLVNHARCPYVRLLRSHCRFRTAAHQVAGAL-------------NTTSPQRLMNLLR 447

Qy        454 QHSSPWQVYGFVRACLRRLVPPGLWGSRHNERRFLRNTKKFISLGKHAKLSLQELTWKMS 513
              ||||||||||::||: :|||||||||||:||| :| |:|||||: ||||||||||
Db        448 LHSSPWQVYGFLQACVGKLVPPGLWGSRHNQRRFFKNVKRFISLGKYDKLSLQELTWKMK 507

Qy        514 VRDCAWLRRSPGVGCVPAAEHRLREEILAKFLHWLMSVYVVELLRSFFYVTETTFQKNRL 573
              |:|| ||| |||  |||||||| || ||| || |||  ||||||||||||||||||||||
Db        508 VQDCRWLRSSPGNNCVPAAEHRTRERILAVFLFWLMDAYVVELLRSFFYVTETTFQKNRL 567

Qy        574 FFYRKSVWSKLQSIGIRQHLKRVQLRELSEAEVRQHREARPALLTSRLRFIPKPDGLRPI 633
              |||||:| :|||||:| ||:||:|:|||: |||| :|| ||:   |||||||| |||||
Db        568 FFYRKSMWRRLQSIGVRHHLERVRLQELSQEEVRQRQEAWPAMPICRLRFIPKPSGLRPI 627

Qy        634 VNMDYVVGARTFRREKRAERLTSRVKALFSVLNYERARRPGLLGASVLGLDDIHRAWRTF 693
              ||| | :| | | : |:|:  |  :| ||||||||  :   |||||||||:||:| ||||
Db        628 VNMSY-MGTRAFDKGKQAQHFTQCLKTLFSVLNYELTKHTNLLGASVLGLNDIYRTWRTF 686

Qy        694 VLRVRAQDPPPELYFVKVDVTGAYDTIPQDRLTEVIASIIK-PQNTYCVRRYAVVQKAAH 752
              |||||  || | :|||| |||||| |||||| |||||::|: | |:||: :|||||:
Db        687 VLRVRTLDPAPRMYFVKADVTGAYDAIPQDKLVEVIANMIRHPDNSYCIHQYAVVQRDRQ 746

Qy        753 GHVRKAFKSHVSTLTDLQPYMRQFVAHLQ--ETSPLRDAVVIEQSSSLNEASSGLFDVFL 810
              | : |:|:  ||||:||||:| ||: |||   :|| ||::|||||| ||||||| ||| ||
Db        747 GQIHKSFRRQVSTLSDLQPHMGQFLKHLQDSDTSALRNSVVIEQSLSLNEASSSLFDFFL 806

Qy        811 RFMCHHAVRIRGKSYVQCQGIPQGSILSTLLCSLCYGDMENKLFAGIRRDGLLLRLVDDF 870
              ||: :  |:| |: |||||||||| |||||||||:|||||||| :::|||||  ||||
Db        807 RFVRNSVVKIGGRCYVQCQGIPQGSSLSTLLCSLCFGDMENKLFAEVQQDGLLLRFVDDF 866

Qy        871 LLVTPHLTHAKTFLRTLVRGVPEYGCVVNLRKTVVNFPVEDEALGGTAFVQMPAHGLFPW 930
              |||||||  |: ||| ||||:||||::||:||||||||:   | |||  |:||| ||||
Db        867 LLVTPHLVQAEAFLRALVRGIPEYGCMINLQKTVVNFPVDAGTLDGTAPHQLPAHCLFPW 926

Qy        931 CGLLLDTRTLEVQSDYSSYARTSIRASLTFNRGFKAGRNMRRKLFGVLRLKCHSLFLDLQ 990
              |||||||:||||  ||: ||||||:||||| | |||||||||:||  ||||||||||||||
Db        927 CGLLLDTQTLEVLCDYTGYARTSIKASLTFQRTFKAGRNMRQKLLAVLRLKCHSLFLDLQ 986

Qy        991 VNSLQTVCTNIYKILLLQAYRFHACVLQLPFHQQVWKNPTFFLRVISDTASLCYSILKAK 1050
              :||||||| |:||| |||||||||| ||||| | | ||| ||| :||: || |||||| |
Db        987 MNSLQTVCINVYKIFLLQAYRFHACALQLPFDQHVRKNPAFFLSIISNIASCCYSILKVK 1046

Qy       1051 NAGMSLGAKGAAGPLPSEAVQWLCHQAFLLKLTRHRVTYVPLLGSLRTAQTQLSRKLPGT 1110
              ||||:| ||||:|  | || :|||:|||||||  | |||  ||| ||||| || ||||
Db       1047 NAGMTLKAKGASGSFPPEAARWLCYQAFLLKLAGHSVTYKCLLGPLRTAQKQLCRKLPRA 1106

Qy       1111 TLTALEAAANPALPSDFKTILD 1132
              |:  || ||:||| :||:||||
Db       1107 TMAILETAADPALSTDFQTILD 1128


RESULT 53
ADG90603
ID   ADG90603 standard; protein; 1128 AA.
XX
AC   ADG90603;
XX
DT   25-MAR-2004  (first entry)
XX
DE   Hamster TERT SEQ ID NO:6.
XX
KW   hamster; immune response; telomerase reverse transcriptase; TERT;
KW   cytostatic; immunostimulant; cancer; cytotoxic T cell response.
XX
OS   Mesocricetus auratus.
XX
PN   WO2004002408-A2.
XX
PD   08-JAN-2004.
XX
PF   24-JUN-2003; 2003WO-US019844.
XX
PR   27-JUN-2002; 2002US-0393295P.
XX
PA   (GERO-) GERON CORP.
XX
PI   Majumdar A,  Ferber IA,  Frolkis M,  Wang Z;
XX
DR   WPI; 2004-071946/07.
DR   N-PSDB; ADG90602.
XX
PT   Eliciting an immune response in a mammal specific for its own telomerase
PT   reverse transcriptase (TERT), useful for treating or preventing cancer,
PT   comprises administering a composition containing TERT of another
PT   mammalian species.
XX
PS   Claim 10; SEQ ID NO 6; 44pp; English.
XX
CC   The invention relates to a novel method for eliciting an immune response
CC   in a mammalian subject that is specific for its own telomerase reverse
CC   transcriptase (TERT), comprising administering an immunogenic composition
CC   containing a protein with at least 20 consecutive amino acids of TERT of
CC   another mammalian species, or a nucleic acid encoding the protein. A
CC   composition of the invention has cytostatic, and immunostimulant
CC   activity. The protein or the nucleic acid encoding the protein is useful
CC   in the manufacture of a medicament for the treatment of cancer in a human
CC   or for eliciting a cytotoxic T cell response in a human.
XX
SQ   Sequence 1128 AA;

  Query Match             60.9%;  Score 3628;  DB 8;  Length 1128;
  Best Local Similarity   63.3%;  Pred. No. 9.8e-296;
  Matches  736;  Conservative  124;  Mismatches  238;  Indels   64;  Gaps   16;

Qy          1 MPRAPRCRAVRSLLRSHYREVLPLATFVRRLGPQGWRLVQRGDPAAFRALVAQCLVCVPW 60
              ||||||||||||:|||| ||:| ||||||||||||:| :||| |||  || |||:|||||||
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Db          1 MPRAPRCRAVRALLRSQYRQVWPLATFVRRLGPEGRQLVQPGDPKVFRTLVARCLVCVPW 60

Qy         61 DARPPPAAPSFRQVSCLKELVARVLQRLCERGAKNVLAFGFALLDGARGGPPEAFTTSVR 120
               |::||||  || ||| |||||||:|||||| :||| ||||||:||:||||  ||||||
Db         61 DSQPPPADLSFHQVSSLKELVARVVQRLCERGERNVLTFGFALLNGAQGGPPMTFTTSVR 120

Qy        121 SYLPNTVTDALRGSGAWGLLLRRVGDDVLVHLLARCALFVLVAPSCAYQVCGPPLYQLGA 180
               |||||:||::|| |||| ||| |||||:||:|||||||::|| |||||||| |||: |
Db        121 SYLPNSVTESLRVSGAWMLLLNRVGDDLLVYLLARCALYLLVPPSCAYQVCGSPLYQICA 180

Qy        181 ATQARPP-PHASGPRRRLG--------CERAWNHSVREAGVPLGLPAPGARRRGGSASRS 231
                 :  |       | | :|          |  | | :||  |  ||:  |:|     :||
Db        181 TAETWPSVSRIYRPTRPVGRNFTHLGSTHRVRNSSHQEAWKPPPLPSREAKRSLSITNRS 240

Qy        232 LPLPKRPRRGAAPEPERTPVGQGSWAHPGRTRGPSDRGFCVVSPAR----PAEEATSLEG 287
               :|  |: |   ||  |: |  |          |||: : | :||:    |    |  |
Db        241 VPPSKKARCDLAPRLEKGPYRQA-------VPTPSDKTW-VPNPAKSHAVPISRTTK-ED 291

Qy        288 ALSGTRHSHPSVGRQ----HHAGPPSTS-RPP--------RPWDTPCPPVYAETKHFLYS 334
               || :   | : |     :   | ||| : |         ||        | ||| ||||
Db        292 LSSGVK--APGLSRSGSVCYKHKPSSTSLQSPLCQNAFQLRP--------YTETKRFLYS 341

Qy        335 -SGDKEQLRPSFLLSSLRPSLTGARRLVETIFLGSRPWMPGTPRRLPRLPQRYWQMRPLF 393
                | :|:| |||||::|:||||||||||| :||| ||   |       || :||||||||
Db        342 REGGRERLNPSFLLNNLQPSLTGARRLVEILFLGMRPRTSGPLCGRRRLSKRYWQMRPLF 401

Qy        394 LELLGNHAQCPYGVLLKTHCPLRAAVTPAAGVCAREKPQGSVAAPEEEDTDPRRLVQLLR 453
               :|| |||:|||  ||::||  | |    ||                | |:||: |||
Db        402 QQLLVNHARCPYVRLLRSHCRFRTAAHQVAGAL-------------NTTSPQRLMNLLR 447

Qy        454 QHSSPWQVYGFVRACLRRLVPPGLWGSRHNERRFLRNTKKFISLGKHAKLSLQELTWKMS 513
               ||||||||||::||: :|||||||||||:||| :| |:||||||: ||||||||||
Db        448 LHSSPWQVYGFLQACVGKLVPPGLWGSRHNQRRFFKNVKRFISLGKYDKLSLQELTWKMK 507

Qy        514 VRDCAWLRRSPGVGCVPAAEHRLREEILAKFLHWLMSVYVVELLRSFFYVTETTFQKNRL 573
               |:|| ||| |||  |||||||| || ||| || |||  |||||||||||||||||||||
Db        508 VQDCRWLRSSPGNNCVPAAEHRTRERILAVFLFWLMDAYVVELLRSFFYVTETTFQKNRL 567

Qy        574 FFYRKSVWSKLQSIGIRQHLKRVQLRELSEAEVRQHREARPALLTSRLRFIPKPDGLRPI 633
               ||||||:| :|||||:| ||:||:|:|||: |||| :|| ||:   |||||||| |||||
Db        568 FFYRKSMWRRLQSIGVRHHLERVRLQELSQEEVRQRQEAWPAMPICRLRFIPKPSGLRPI 627

Qy        634 VNMDYVVGARTFRREKRAERLTSRVKALFSVLNYERARRPGLLGASVLGLDDIHRAWRTF 693
               ||| | :| | | : |:|:  |  :| ||||||||  :   |||||||||:||:| ||||
Db        628 VNMSY-MGTRAFDKGKQAQHFTQCLKTLFSVLNYELTKHTNLLGASVLGLNDIYRTWRTF 686

Qy        694 VLRVRAQDPPPELYFVKVDVTGAYDTIPQDRLTEVIASIIK-PQNTYCVRRYAVVQKAAH 752
               |||||  || | :|||| ||||||| ||||:| ||||::|: | |:||: :|||||:
Db        687 VLRVRTLDPAPRMYFVKADVTGAYDAIPQDKLVEVIANMIRHPDNSYCIHQYAVVQRDRQ 746

Qy        753 GHVRKAFKSHVSTLTDLQPYMRQFVAHLQ--ETSPLRDAVVIEQSSSLNEASSGLFDVFL 810
               | : |:|:  ||||:||||:| ||: |||  :|| ||::|||||| ||||||| ||| ||
Db        747 GQIHKSFRRQVSTLSDLQPHMGQFLKHLQDSDTSALRNSVVIEQSLSLNEASSSLFDFFL 806

Qy        811 RFMCHHAVRIRGKSYVQCQGIPQGSILSTLLCSLCYGDMENKLFAGIRRDGLLLRLVDDF 870
               ||: :  |:| |: |||||||||| ||||||||:|||||||| :::|||||| ||||
Db        807 RFVRNSVVKIGGRCYVQCQGIPQGSSLSTLLCSLCFGDMENKLFAEVQQDGLLLRFVDDF 866

Qy        871 LLVTPHLTHAKTFLRTLVRGVPEYGCVVNLRKTVVNFPVEDEALGGTAFVQMPAHGLFPW 930
               |||||||  |: ||| |||||||||::||:||||||||:   | |||  |:||| ||||
Db        867 LLVTPHLVQAEAFLRALVRGIPEYGCMINLQKTVVNFPVDAGTLDGTAPHQLPAHCLFPW 926

Qy        931 CGLLLDTRTLEVQSDYSSYARTSIRASLTFNRGFKAGRNMRRKLFGVLRLKCHSLFLDLQ 990
               |||||||:|||| ||: |||||||:||||| | |||||||:||  ||||||||||||||
Db        927 CGLLLDTQTLEVLCDYTGYARTSIKASLTFQRTFKAGRNMRQKLLAVLRLKCHSLFLDLQ 986

Qy        991 VNSLQTVCTNIYKILLLQAYRFHACVLQLPFHQQVWKNPTFFLRVISDTASLCYSILKAK 1050
               :||||||| |:||| |||||||||| ||||| | | ||| ||| :||: || |||||| |
Db        987 MNSLQTVCINVYKIFLLQAYRFHACALQLPFDQHVRKNPAFFLSIISNIASCCYSILKVK 1046

Qy       1051 NAGMSLGAKGAAGPLPSEAVQWLCHQAFLLKLTRHRVTYVPLLGSLRTAQTQLSRKLPGT 1110
               ||||:| ||||:|  | || :|||:|||||||  | |||  ||| ||||| || ||||
Db       1047 NAGMTLKAKGASGSFPPEAARWLCYQAFLLKLAGHSVTYKCLLGPLRTAQKQLCRKLPRA 1106

Qy       1111 TLTALEAAANPALPSDFKTILD 1132
                 |:  || ||:||| :||:||||
Db       1107 TMAILETAADPALSTDFQTILD 1128
```

RESULT 54
AAY26579
ID AAY26579 standard; protein; 1122 AA.
XX
AC AAY26579;
XX
DT 13-SEP-1999 (first entry)
XX
DE Murine telomerase reverse transcriptase (mTERT) enzyme.
XX
KW Telomerase reverse transcriptase; TERT; mouse; telomere length assay;
KW immunogen; enzyme; telomerase-mediated DNA replication.
XX
OS Mus sp.
XX
PN WO9927113-A1.
XX
PD 03-JUN-1999.
XX
PF 25-NOV-1998; 98WO-US025211.
XX
PR 26-NOV-1997; 97US-00979742.
PR 16-MAR-1998; 98US-00042460.
XX
PA (GERO-) GERON CORP.
PA (YESH) UNIV YESHIVA EINSTEIN COLLEGE.
XX
PI Morin GB, Allsopp R, Depinho R, Greenberg R;
XX
DR WPI; 1999-347722/29.
DR N-PSDB; AAX80994.
XX
PT Mouse telomerase reverse transcriptase (mTERT) enzyme proteins and
PT nucleic acids.
XX
PS Claim 8; Fig 2; 135pp; English.
XX
CC The invention relates to a mouse telomerase reverse transcriptase (mTERT)
CC enzyme. Compositions containing mTERT can be used in telomere length
CC assays. Isolated mTERT is useful as an immunogen for the production of
CC monoclonal or polyclonal antibodies. The method is useful for assessing
CC the degree of purification and identification of new mTERT species, such
CC as an mTERT allele, homolog or isoform, or to screen for modulators
CC (antagonists and agonists) of telomerase-mediated DNA replication.
CC Antagonists and agonists of mTERT can be used to modify the activity of
CC other telomerase enzymes such as human TERT (hTERT). The present sequence
CC represents a mTERT enzyme
XX
SQ Sequence 1122 AA;

Query Match 58.8%; Score 3505; DB 2; Length 1122;
Best Local Similarity 62.4%; Pred. No. 2.2e-285;
Matches 719; Conservative 122; Mismatches 260; Indels 52; Gaps 13;

```
Qy          1 MPRAPRCRAVRSLLRSHYREVLPLATFVRRLGPQGWRLVQRGDPAAFRALVAQCLVCVPW 60
              | ||||| |||||||| |||| |||||||||||:| |||| |||  :| |||||||: |
Db          1 MTRAPRCPAVRSLLRSRYREVWPLATFVRRLGPEGRRLVQPGDPKIYRTLVAQCLVCMHW 60

Qy         61 DARPPPAAPSFRQVSCLKELVARVLQRLCERGAKNVLAFGFALLDGARGGPPEAFTTSVR 120
               ::||||  || ||| |||||||:||||||  :||||||| ||: ||| |||  :|||
Db         61 GSQPPPADLSFHQVSSLKELVARVVQRLCERNERNVLAFGFELLNEARGGPPMAFTSSVR 120

Qy        121 SYLPNTVTDALRGSGAWGLLLRRVGDDVLVHLLARCALFVLVAPSCAYQVCGPPLYQLGA 180
               |||||| : || |||| ||| |||||:||:||| |||::|| |||||||| ||||: |
Db        121 SYLPNTVIETLRVSGAWMLLLSRVGDDLLVYLLAHCALYLLVPPSCAYQVCGSPLYQICA 180

Qy        181 ATQARPPPHAS-GPRRRLG--------CERAWNHSVREAGVPLGLPAPGARRRGGSASRS 231
```

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Db        181 TTDIWPSVSASYRPTRPVGRNFTNLRFLQQIKSSSRQEAPKPLALPSRGTKRHLSLTSTS 240

Qy        232 LPLPKRPRRGAAPEPERTPVGQGSWAHPGRTRGPSDRGFCVVSPAR-----PAEEATSLE 286

Db        241 VPSAKKARCYPVPRVEEGP-------HRQVLPTPSGKSW-VPSPARSPEVPTAEKDLSSK 292

Qy        287 GALSGTRHSHPSVGRQHHAGPPSTSRPPRPWDTPCPPVYAETKHFLYSSGD-KEQLRPSF 345

Db        293 GKVSDLSLS-GSVCCKHKPSSTSLLSPPRQNAFQLRP-FIETRHFLYSRGDGQERLNPSF 350

Qy        346 LLSSLRPSLTGARRLVETIFLGSRPWMPGTPRRLPRLPQRYWQMRPLFLELLGNHAQCPY 405

Db        351 LLSNLQPNLTGARRLVEIIFLGSRPRTSGPLCRTHRLSRRYWQMRPLFQQLLVNHAECQY 410

Qy        406 GVLLKTHCPLRAA---VTPAAGVCAREKPQGSVAAPEEEDTDPRRLVQLLRQHSSPWQVY 462

Db        411 VRLLRSHCRFRTANQQVTDAL-----------------NTSPPHLMDLLRLHSSPWQVY 452

Qy        463 GFVRACLRRLVPPGLWGSRHNERRFLRNTKKFISLGKHAKLSLQELTWKMSVRDCAWLRR 522

Db        453 GFLRACLCKVVSASLWGTRHNERRFFKNLKKFISLGKYGKLSLQELMWKMKVEDCHWLRS 512

Qy        523 SPGVGCVPAAEHRLREEILAKFLHWLMSVYVVELLRSFFYVTETTFQKNRLFFYRKSVWS 582

Db        513 SPGKDRVPAAEHRLRERILATFLFWLMDTYVVQLLRSFFYITESTFQKNRLFFYRKSVWS 572

Qy        583 KLQSIGIRQHLKRVQLRELSEAEVRQHREARPALLTSRLRFIPKPDGLRPIVNMDYVVGA 642

Db        573 KLQSIGVRQHLERVRLRELSQEEVRHHQDTWLAMPICRLRFIPKPNGLRPIVNMSYSMGT 632

Qy        643 RTFRREKRAERLTSRVKALFSVLNYERARRPGLLGASVLGLDDIHRAWRTFVLRVRAQDP 702

Db        633 RALGRRKQAQHFTQRLKTLFSMLNYERTKHPHLMGSSVLGMNDIYRTWRAFVLRVRALDQ 692

Qy        703 PPELYFVKVDVTGAYDTIPQDRLTEVIASIIK-PQNTYCVRRYAVVQKAAHGHVRKAFKS 761

Db        693 TPRMYFVKADVTGAYDAIPQGKLVEVVANMIRHSESTYCIRQYAVVRRDSQGQVHKSFRR 752

Qy        762 HVSTLTDLQPYMRQFVAHLQET--SPLRDAVVIEQSSSLNEASSGLFDVFLRFMCHHAVR 819

Db        753 QVTTLSDLQPYMGQFLKHLQDSDASALRNSVVIEQSISMNESSSSLFDFFLHFLRHSVVK 812

Qy        820 IRGKSYVQCQGIPQGSILSTLLCSLCYGDMENKLFAGIRRDGLLLRLVDDFLLVTPHLTH 879

Db        813 IGDRCYTQCQGIPQGSSLSTLLCSLCFGDMENKLFAEVQRDGLLLRFVDDFLLVTPHLDQ 872

Qy        880 AKTFLRTLVRGVPEYGCVVNLRKTVVNFPVEDEALGGTAFVQMPAHGLFPWCGLLLDTRT 939

Db        873 AKTFLSTLVHGVPEYGCMINLQKTVVNFPVEPGTLGGAAPYQLPAHCLFPWCGLLLDTQT 932

Qy        940 LEVQSDYSSYARTSIRASLTFNRGFKAGRNMRRKLFGVLRLKCHSLFLDLQVNSLQTVCT 999

Db        933 LEVFCDYSGYAQTSIKTSLTFQSVFKAGKTMRNKLLSVLRLKCHGLFLDLQVNSLQTVCI 992

Qy       1000 NIYKILLLQAYRFHACVLQLPFHQQVWKNPTFFLRVISDTASLCYSILKAKNAGMSLGAK 1059

Db        993 NIYKIFLLQAYRFHACVIQLPFDQRVRKNLTFFLGIISSQASCCYAILKVKNPGMTLKAS 1052

Qy       1060 GAAGPLPSEAVQWLCHQAFLLKLTRHRVTYVPLLGSLRTAQTQLSRKLPGTTLTALEAAA 1119

Db       1053 GS---FPPEAAHWLCYQAFLLKLAAHSVIYKCLLGPLRTAQKLLCRKLPEATMTILKAAA 1109

Qy       1120 NPALPSDFKTILD 1132

Db       1110 DPALSTDFQTILD 1122


RESULT 55
ADG90601
ID   ADG90601 standard; protein; 1122 AA.
XX
AC   ADG90601;
XX
DT   25-MAR-2004  (first entry)
XX
DE   Murine TERT SEQ ID NO:4.
XX
KW   mouse; immune response; telomerase reverse transcriptase; TERT;
KW   cytostatic; immunostimulant; cancer; cytotoxic T cell response.
XX
OS   Mus sp.
XX
PN   WO2004002408-A2.
XX
PD   08-JAN-2004.
XX
PF   24-JUN-2003; 2003WO-US019844.
XX
PR   27-JUN-2002; 2002US-0393295P.
XX
PA   (GERO-) GERON CORP.
XX
PI   Majumdar A,  Ferber IA,  Frolkis M,  Wang Z;
XX
DR   WPI; 2004-071946/07.
DR   N-PSDB; ADG90600.
XX
PT   Eliciting an immune response in a mammal specific for its own telomerase
PT   reverse transcriptase (TERT), useful for treating or preventing cancer,
PT   comprises administering a composition containing TERT of another
PT   mammalian species.
XX
PS   Claim 10; SEQ ID NO 4; 44pp; English.
XX
CC   The invention relates to a novel method for eliciting an immune response
CC   in a mammalian subject that is specific for its own telomerase reverse
CC   transcriptase (TERT), comprising administering an immunogenic composition
CC   containing a protein with at least 20 consecutive amino acids of TERT of
CC   another mammalian species, or a nucleic acid encoding the protein. A
CC   composition of the invention has cytostatic, and immunostimulant
CC   activity. The protein or the nucleic acid encoding the protein is useful
CC   in the manufacture of a medicament for the treatment of cancer in a human
CC   or for eliciting a cytotoxic T cell response in a human.
XX
SQ   Sequence 1122 AA;

  Query Match             58.8%;  Score 3505;  DB 8;  Length 1122;
  Best Local Similarity   62.4%;  Pred. No. 2.2e-285;
  Matches  719;  Conservative  122;  Mismatches  260;  Indels   52;  Gaps   13;

Qy          1 MPRAPRCRAVRSLLRSHYREVLPLATFVRRLGPQGWRLVQRGDPAAFRALVAQCLVCVPW 60

Db          1 MTRAPRCPAVRSLLRSRYREVWPLATFVRRLGPEGRRLVQPGDPKIYRTLVAQCLVCMHW 60

Qy         61 DARPPPAAPSFRQVSCLKELVARVLQRLCERGAKNVLAFGFALLDGARGGPPEAFTTSVR 120

Db         61 GSQPPPADLSFHQVSSLKELVARVVQRLCERNERNVLAFGFELLNEARGGPPMAFTSSVR 120

Qy        121 SYLPNTVTDALRGSGAWGLLLRRVGDDVLVHLLARCALFVLVAPSCAYQVCGPPLYQLGA 180

Db        121 SYLPNTVIETLRVSGAWMLLLSRVGDDLLVYLLAHCALYLLVPPSCAYQVCGSPLYQICA 180

Qy        181 ATQARPPPHAS-GPRRRLG--------CERAWNHSVREAGVPLGLPAPGARRRGGSASRS 231

Db        181 TTDIWPSVSASYRPTRPVGRNFTNLRFLQQIKSSSRQEAPKPLALPSRGTKRHLSLTSTS 240

Qy        232 LPLPKRPRRGAAPEPERTPVGQGSWAHPGRTRGPSDRGFCVVSPAR-----PAEEATSLE 286

Db        241 VPSAKKARCYPVPRVEEGP-------HRQVLPTPSGKSW-VPSPARSPEVPTAEKDLSSK 292

Qy        287 GALSGTRHSHPSVGRQHHAGPPSTSRPPRPWDTPCPPVYAETKHFLYSSGD-KEQLRPSF 345

Db        293 GKVSDLSLS-GSVCCKHKPSSTSLLSPPRQNAFQLRP-FIETRHFLYSRGDGQERLNPSF 350

Qy        346 LLSSLRPSLTGARRLVETIFLGSRPWMPGTPRRLPRLPQRYWQMRPLFLELLGNHAQCPY 405
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Db        351 LLSNLQPNLTGARRLVEIIFLGSRPRTSGPLCRTHRLSRRYWQMRPLFQQLLVNHAECQY 410

Qy        406 GVLLKTHCPLRAA---VTPAAGVCAREKPQGSVAAPEEEDTDPRRLVQLLRQHSSPWQVY 462

Db        411 VRLLRSHCRFRTANQQVTDAL-----------------NTSPPHLMDLLRLHSSPWQVY 452

Qy        463 GFVRACLRRLVPPGLWGSRHNERRFLRNTKKFISLGKHAKLSLQELTWKMSVRDCAWLRR 522

Db        453 GFLRACLCKVVSASLWGTRHNERRFFKNLKKFISLGKYGKLSLQELMWKMKVEDCHWLRS 512

Qy        523 SPGVGCVPAAEHRLREEILAKFLHWLMSVYVVELLRSFFYVTETTFQKNRLFFYRKSVWS 582

Db        513 SPGKDRVPAAEHRLRERILATFLFWLMDTYVVQLLRSFFYITESTFQKNRLFFYRKSVWS 572

Qy        583 KLQSIGIRQHLKRVQLRELSEAEVRQHREARPALLTSRLRFIPKPDGLRPIVNMDYVVGA 642

Db        573 KLQSIGVRQHLERVRLRELSQEEVRHHQDTWLAMPICRLRFIPKPNGLRPIVNMSYSMGT 632

Qy        643 RTFRREKRAERLTSRVKALFSVLNYERARRPGLLGASVLGLDDIHRAWRTFVLRVRAQDP 702

Db        633 RALGRRKQAQHFTQRLKTLFSMLNYERTKHPHLMGSSVLGMNDIYRTWRAFVLRVRALDQ 692

Qy        703 PPELYFVKVDVTGAYDTIPQDRLTEVIASIIK-PQNTYCVRRYAVVQKAAHGHVRKAFKS 761

Db        693 TPRMYFVKADVTGAYDAIPQGKLVEVVANMIRHSESTYCIRQYAVVRRDSQGQVHKSFRR 752

Qy        762 HVSTLTDLQPYMRQFVAHLQET--SPLRDAVVIEQSSSLNEASSGLFDVFLRFMCHHAVR 819

Db        753 QVTTLSDLQPYMGQFLKHLQDSDASALRNSVVIEQSISMNESSSSLFDFFLHFLRHSVVK 812

Qy        820 IRGKSYVQCQGIPQGSILSTLLCSLCYGDMENKLFAGIRRDGLLLRLVDDFLLVTPHLTH 879

Db        813 IGDRCYTQCQGIPQGSSLSTLLCSLCFGDMENKLFAEVQRDGLLLRFVDDFLLVTPHLDQ 872

Qy        880 AKTFLRTLVRGVPEYGCVVNLRKTVVNFPVEDEALGGTAFVQMPAHGLFPWCGLLLDTRT 939

Db        873 AKTFLSTLVHGVPEYGCMINLQKTVVNFPVEPGTLGGAAPYQLPAHCLFPWCGLLLDTQT 932

Qy        940 LEVQSDYSSYARTSIRASLTFNRGFKAGRNMRRKLFGVLRLKCHSLFLDLQVNSLQTVCT 999

Db        933 LEVFCDYSGYAQTSIKTSLTFQSVFKAGKTMRNKLLSVLRLKCHGLFLDLQVNSLQTVCI 992

Qy       1000 NIYKILLLQAYRFHACVLQLPFHQQVWKNPTFFLRVISDTASLCYSILKAKNAGMSLGAK 1059

Db        993 NIYKIFLLQAYRFHACVIQLPFDQRVRKNLTFFLGIISSQASCCYAILKVKNPGMTLKAS 1052

Qy       1060 GAAGPLPSEAVQWLCHQAFLLKLTRHRVTYVPLLGSLRTAQTQLSRKLPGTTLTALEAAA 1119

Db       1053 GS---FPPEAAHWLCYQAFLLKLAAHSVIYKCLLGPLRTAQKLLCRKLPEATMTILKAAA 1109

Qy       1120 NPALPSDFKTILD 1132

Db       1110 DPALSTDFQTILD 1122


RESULT 56
ABB06711
ID   ABB06711 standard; protein; 1122 AA.
XX
AC   ABB06711;
XX
DT   11-JUN-2002  (first entry)
XX
DE   Mouse telomerase protein sequence.
XX
KW   Mouse; telomerase; promoter; telomerase catalyst subunit; TERT; mTERT;
KW   enzyme; transgenic mouse; drug development; anticancer.
XX
OS   Mus sp.
XX
PN   JP2002000121-A.
XX
PD   08-JAN-2002.
XX
PF   23-JUN-2000; 2000JP-00190137.
XX
PR   23-JUN-2000; 2000JP-00190137.
XX
PA   (RIKO-) ZH RIKOGAKU SHINKOKAI.
PA   (KIRI ) KIRIN BREWERY KK.
XX
DR   WPI; 2002-298279/34.
XX
PT   A transgenic mouse comprising a DNA promoter region of mouse telomerase
PT   catalyst subunit (TERT) is used for the development of drugs and
PT   anticancer agents for regeneration of tissues and organs.
XX
PS   Disclosure; Fig 3; 13pp; Japanese.
XX
CC   The present invention describes a transgenic mouse (I) comprising a DNA
CC   construct having a DNA containing a promoter region of mouse telomerase
CC   catalyst subunit (TERT) and a DNA containing a reporter gene connected
CC   under the control of the promoter region. The transgenic mouse can be
CC   used in the development of drugs and anticancer agents for regeneration
CC   of tissues and organs. The present sequence represents the mouse
CC   telomerase protein, which is given in the exemplification of the present
CC   invention
XX
SQ   Sequence 1122 AA;

  Query Match           58.3%;  Score 3475;  DB 5;  Length 1122;
  Best Local Similarity  61.9%;  Pred. No. 7.4e-283;
  Matches  714;  Conservative  121;  Mismatches  266;  Indels   52;  Gaps   12;

Qy          1 MPRAPRCRAVRSLLRSHYREVLPLATFVRRLGPQGWRLVQRGDPAAFRALVAQCLVCVPW 60

Db          1 MTRAPRCPAVRSLLRSRYREVWPLATFVRRLGPEGRRLVQPGDPKIYRTLVAQCLVCMHW 60

Qy         61 DARPPPAAPSFRQVSCLKELVARVLQRLCERGAKNVLAFGFALLDGARGGPPEAFTTSVR 120

Db         61 GSQPPPADLSFHQVSSLKELVARVVQRLCERNERNVLAFGFELLNEARGGPPMAFTSSVR 120

Qy        121 SYLPNTVTDALRGSGAWGLLLRRVGDDVLVHLLARCALFVLVAPSCAYQVCGPPLYQLGA 180

Db        121 SYLPNTVIETLRVSGAWMLLLSRVGDDLLVYLLAHCALYLLVPPSCAYQVCGSPLYQICA 180

Qy        181 ATQARPPPHAS-GPRRRLG--------CERAWNHSVREAGVPLGLPAPGARRRGGSASRS 231

Db        181 TTDIWPSVSASYRPTRPVGRNFTNLRFLQQIKSSSRQEAPKPLALPSRGTKRHLSLTSTS 240

Qy        232 LPLPKRPRRGAAPEPERTPVGQGSWAHPGRTRGPSDRGFCVVSPAR-----PAEEATSLE 286

Db        241 VPSAKKARCYPVPRVEEGPHRQVLPTFSGKSWVP--------SPARSPEVPTAEKDLSSK 292

Qy        287 GALSGTRHSHPSVGRQHHAGPPSTSRPPRPWDTPCPPVYAETKHFLYSSGD-KEQLRPSF 345

Db        293 GKVSDLSLS-GSVCCKHKPSSTSLLSPPRQNAFQLRP-FIETRHFLYSRGDGQERLNPSF 350

Qy        346 LLSSLRPSLTGARRLVETIFLGSRPWMPGTPRRLPRLPQRYWQMRPLFLELLGNHAQCPY 405

Db        351 LLSNLQPNLTGARRLVEIIFLGSRPRTSGPLCRTHRLSHRYWQMRPLFQQLLVNHAECQY 410

Qy        406 GVLLKTHCPLRAA---VTPAAGVCAREKPQGSVAAPEEEDTDPRRLVQLLRQHSSPWQVY 462

Db        411 VRLLRSHCRFRTANQQVTDAL-----------------NTSPPHLMDLLRLHSSPWQVY 452

Qy        463 GFVRACLRRLVPPGLWGSRHNERRFLRNTKKFISLGKHAKLSLQELTWKMSVRDCAWLRR 522

Db        453 GFLRACLCKVVSASLWGTRHNEHRFFKNLKKFISLGKYGKLSLQELMWKMKVEDCHWLRS 512

Qy        523 SPGVGCVPAAEHRLREEILAKFLHWLMSVYVVELLRSFFYVTETTFQKNRLFFYRKSVWS 582

Db        513 SPGKDRVPAAEHRLRERILATFLFWLMDTYVVQLLRSPFYITESTFQKNRLFFYRKSVWS 572

Qy        583 KLQSIGIRQHLKRVQLRELSEAEVRQHREARPALLTSRLRFIPKPDGLRPIVNMDYVVGA 642
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                ||||||:||||:||:|| ||: ||| |::   |:   ||||||||:||||||| | :|
Db        573 KLQSIGVRQHLERVRLRSLSQEEVRHHQDTWLAMPICRLRFIPKPNGLRPIVNMSYSMGT 632

Qy        643 RTFRREKRAERLTSRVKALFSVLNYERARRPGLLGASVLGLDDIHRAWRTFVLRVRAQDP 702
              |   | |:|:  | |:| |||:||||| : | |:|:||||::||:| || |||||||
Db        633 RALGRRKQAQHFTQRLKTLFSMLNYERTKHPHLMGSSVLGMNDIYRTWRAFVLRVRALDQ 692

Qy        703 PPELYFVKVDVTGAYDTIPQDRLTEVIASIIK-PQNTYCVRRYAVVQKAAHGHVRKAFKS 761
               | :|||| ||||||| ||| :| ||:|::|:  ::|||:|:||||:: : | | |:|:
Db        693 TPRMYFVKADVTGAYDAIPQGKLVEVVANMIRHSESTYCIRQYAVVRRDSQGQVHKSFRR 752

Qy        762 HVSTLTDLQPYMRQFVAHLQET--SPLRDAVVIEQSSSLNEASSGLFDVFLRFMCHHAVR 819
              |:||:|||||| ||: |||::  | ||::|||||| |:||:|| ||| || |: |  |:
Db        753 QVTTLSDLQPYMGQFLKHLQDSDASALRNSVVIEQSISMNESSSSLFDFFLHFLRHSVVK 812

Qy        820 IRGKSYVQCQGIPQGSILSTLLCSLCYGDMENKLFAGIRRDGLLLRLVDDFLLVTPHLTH 879
              |  : | ||||||||| |||||||||:||||||||| ::|||||| |||||||||||
Db        813 IGDRCYTQCQGIPQGSSLSTLLCSLCFGDMENKLFAKVQRDGLLLRFVDDFLLVTPHLDQ 872

Qy        880 AKTFLRTLVRGVPEYGCVVNLRKTVVNFPVEDEALGGTAFVQMPAHGLFPWCGLLLDTRT 939
              ||||| ||| |||||||::||:|||||||||   ||| |  |:||| ||||||||||:|
Db        873 AKTFLSTLVHGVPEYGCMINLQKTVVNFPVEPGTLGGAAPYQLPAHCLFPWCGLLLDTQT 932

Qy        940 LEVQSDYSSYARTSIRASLTFNRGFKAGRNMRRKLFGVLRLKCHSLFLDLQVNSLQTVCT 999
              |||  ||| ||:|||: ||||   ||||: || ||  ||||||| ||||||||||||||
Db        933 LEVFCDYSGYAQTSIKTSLTFQSVFKAGKTMRNKLLSVLRLKCHGLFLDLQVNSLQTVCI 992

Qy       1000 NIYKILLLQAYRFHACVLQLPFHQQVWKNPTFFLRVISDTASLCYSILKAKNAGMSLGAK 1059
              ||||| |||||||||||:|||| |:| || |||| :||  || ||:||| || | :| |
Db        993 NIYKIFLLQAYRFHACVIQLPFDQRVRKNLTFFLGIISSQASCCYAILKVKNPGNTLKAS 1052

Qy       1060 GAAGPLPSEAVQWLCHQAFLLKLTRHRVTYVPLLGSLRTAQTQLSRKLPGTTLTALEAAA 1119
              |:    | ||  |||:|||||||  | | |  ||| |||||  | ||||  |:| |:|||
Db       1053 GS---FPPEAAHWLCYQAFLLKLAAHSVIYKCLLGPLRTAQKLLCRKLPEATMTILKAAA 1109

Qy       1120 NPALPSDFKTILD 1132
              :||| :||:||||
Db       1110 DPALSTDFQTILD 1122


RESULT 57
AAY00636
ID   AAY00636 standard; protein; 617 AA.
XX
AC   AAY00636;
XX
DT   26-JUL-1999  (first entry)
XX
DE   N-terminal truncated telomerase protein sequence.
XX
KW   Telomerase; human; cancer; diagnosis; melanoma; skin cancer; leukaemia;
KW   neuroblastoma; breast carcinoma; colon carcinoma; lymphoma; osteosarcoma;
KW   smooth muscle cell hyperplasia; stem cell proliferation; Wilm's tumour;
KW   stem cell differentiation; organ regeneration; organ differentiation.
XX
OS   Homo sapiens.
OS   Synthetic.
XX
PN   WO9901560-A1.
XX
PD   14-JAN-1999.
XX
PF   01-JUL-1998;   98WO-US013835.
XX
PR   01-JUL-1997;   97US-0051410P.
PR   21-JUL-1997;   97US-0053018P.
PR   21-JUL-1997;   97US-0053329P.
PR   04-AUG-1997;   97US-0054642P.
PR   09-SEP-1997;   97US-0058287P.
XX
PA   (CAMB-) CAMBIA BIOSYSTEMS LLC.
XX
PI   Kilian A,  Bowtell D;
XX
DR   WPI; 1999-106060/09.
DR   N-PSDB; AAX18264.
XX
PT   New isolated vertebrate telomerase genes - used to develop products for
PT   treating cancers or for organ regeneration, nerve cell or brain cell
PT   growth following injury or bone marrow transplantation.
XX
PS   Claim 4; Fig 11b-c; 134pp; English.
XX
CC   This sequence is a truncated human telomerase of the invention. Primers
CC   that amplify the telomerase coding sequence can be used in a method for
CC   diagnosing cancer in a patient. The telomerase can be used for detection,
CC   diagnosis and drug screening. Inhibitors of telomerase activity can be
CC   used to treat cancers such as melanomas, other skin cancers,
CC   neuroblastomas, breast carcinomas, colon carcinomas, leukaemias,
CC   lymphomas, osteosarcomas or smooth muscle cell hyperplasias or skin
CC   growths. Enhancers of telomerase may be used to stimulate stem cell
CC   proliferation and differentiation (expansion of haematopoietic stem cells
CC   could be administered in the bone marrow transplant context). As well,
CC   many tissues have stem cells. Proliferation of these cells may be useful
CC   in wound healing, hair growth, treatment of disease such as Wilm's
CC   tumour, organ regeneration or differentiation after injury or diseases,
CC   nerve cell or brain cell growth following injury. Note: The C-terminus of
CC   this sequence can be replaced by the sequence shown in AAY00653
XX
SQ   Sequence 617 AA;

  Query Match             54.3%;  Score 3238;  DB 2;  Length 617;
  Best Local Similarity   93.8%;  Pred. No. 2.9e-263;
  Matches  610;  Conservative    0;  Mismatches    0;  Indels   40;  Gaps    1;

Qy          1 MPRAPRCRAVRSLLRSHYREVLPLATFVRRLGPQGWRLVQRGDPAAFRALVAQCLVCVPW 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 MPRAPRCRAVRSLLRSHYREVLPLATFVRRLGPQGWRLVQRGDPAAFRALVAQCLVCVPW 60

Qy         61 DARPPPAAPSFRQVSCLKELVARVLQRLCERGAKNVLAFGFALLDGARGGPPEAFTTSVR 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 DARPPPAAPSFRQVSCLKELVARVLQRLCERGAKNVLAFGFALLDGARGGPPEAFTTSVR 120

Qy        121 SYLPNTVTDALRGSGAWGLLLRRVGDDVLVHLLARCALFVLVAPSCAYQVCGPPLYQLGA 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 SYLPNTVTDALRGSGAWGLLLRRVGDDVLVHLLARCALFVLVAPSCAYQVCGPPLYQLGA 180

Qy        181 ATQARPPPHASGPRRRLGCERAWNHSVREAGVPLGLPAPGARRRGGSASRSLPLPKRPRR 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 ATQARPPPHASGPRRRLGCERAWNHSVREAGVPLGLPAPGARRRGGSASRSLPLPKRPRR 240

Qy        241 GAAPEPERTPVGQGSWAHPGRTRGPSDRGFCVVSPARPAEEATSLEGALSGTRHSHPSVG 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 GAAPEPERTPVGQGSWAHPGRTRGPSDRGFCVVSPARPAEEATSLEGALSGTRHSHPSVG 300

Qy        301 RQHHAGPPSTSRPPRPWDTPCPPVYAETKHFLYSSGDKEQLRPSFLLSSLRPSLTGARRL 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 RQHHAGPPSTSRPPRPWDTPCPPVYAETKHFLYSSGDKEQLRPSFLLSSLRPSLTGARRL 360

Qy        361 VETIFLGSRPWMPGTPRRLPRLPQRYWQMRPLFLELLGNHAQCPYGVLLKTHCPLRAAVT 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        361 VETIFLGSRPWMPGTPRRLPRLPQRYWQMRPLFLELLGNHAQCPYGVLLKTHCPLRAAVT 420

Qy        421 PAAGVCAREKPQGSVAAPEEEDTDPRRLVQLLRQHSSPWQVYGFVRACLRRLVPPGLWGS 480
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        421 PAAGVCAREKPQGSVAAPEEEDTDPRRLVQLLRQHSSPWQVYGFVRACLRRLVPPGLWGS 480

Qy        481 RHNERRFLRNTKKFISLGKHAKLSLQELTWKMSVRDCAWLRRSPGVGCVPAAEHRLREEI 540
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        481 RHNERRFLRNTKKFISLGKHAKLSLQELTWKMSVRDCAWLRRSPGVGCVPAAEHRLREEI 540

Qy        541 LAKFLHWLMSVYVVELLRSFFYVTETTFQKNRLFFYRKSVWSKLQSIGIRQHLKRVQLRE 600
              ||||||||                                        ||||||||||||
Db        541 LAKFLHWL----------------------------------------IRQHLKRVQLRE 560

Qy        601 LSEAEVRQHREARPALLTSRLRFIPKPDGLRPIVNMDYVVGARTFRREKR 650
```

```
                 ||||||||||||||||||||||||||||||||||||||||||||||||||
Db        561 LSEAEVRQHREARPALLTSRLRFIPKPDGLRPIVNMDYVVGARTFRREKR 610


RESULT 58
AAY00635
ID   AAY00635 standard; protein; 588 AA.
XX
AC   AAY00635;
XX
DT   26-JUL-1999  (first entry)
XX
DE   N-terminal truncated telomerase protein sequence.
XX
KW   Telomerase; human; cancer; diagnosis; melanoma; skin cancer; leukaemia;
KW   neuroblastoma; breast carcinoma; colon carcinoma; lymphoma; osteosarcoma;
KW   smooth muscle cell hyperplasia; stem cell proliferation; Wilm's tumour;
KW   stem cell differentiation; organ regeneration; organ differentiation.
XX
OS   Homo sapiens.
OS   Synthetic.
XX
PN   WO9901560-A1.
XX
PD   14-JAN-1999.
XX
PF   01-JUL-1998;   98WO-US013835.
XX
PR   01-JUL-1997;   97US-0051410P.
PR   21-JUL-1997;   97US-0053018P.
PR   21-JUL-1997;   97US-0053329P.
PR   04-AUG-1997;   97US-0054642P.
PR   09-SEP-1997;   97US-0058287P.
XX
PA   (CAMB-) CAMBIA BIOSYSTEMS LLC.
XX
PI   Kilian A,  Bowtell D;
XX
DR   WPI; 1999-106060/09.
DR   N-PSDB; AAX18263.
XX
PT   New isolated vertebrate telomerase genes - used to develop products for
PT   treating cancers or for organ regeneration, nerve cell or brain cell
PT   growth following injury or bone marrow transplantation.
XX
PS   Claim 4; Fig 11a; 134pp; English.
XX
CC   This sequence is a truncated human telomerase of the invention. Primers
CC   that amplify the telomerase coding sequence can be used in a method for
CC   diagnosing cancer in a patient. The telomerase can be used for detection,
CC   diagnosis and drug screening. Inhibitors of telomerase activity can be
CC   used to treat cancers such as melanomas, other skin cancers,
CC   neuroblastomas, breast carcinomas, colon carcinomas, leukaemias,
CC   lymphomas, osteosarcomas or smooth muscle cell hyperplasias or skin
CC   growths. Enhancers of telomerase may be used to stimulate stem cell
CC   proliferation and differentiation (expansion of haematopoietic stem cells
CC   could be administered in the bone marrow transplant context). As well,
CC   many tissues have stem cells. Proliferation of these cells may be useful
CC   in wound healing, hair growth, treatment of disease such as Wilm's
CC   tumour, organ regeneration or differentiation after injury or diseases,
CC   nerve cell or brain cell growth following injury
XX
SQ   Sequence 588 AA;

  Query Match             53.0%;  Score 3160;  DB 2;  Length 588;
  Best Local Similarity   100.0%;  Pred. No. 9.9e-257;
  Matches  588;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 MPRAPRCRAVRSLLRSHYREVLPLATFVRRLGPQGWRLVQRGDPAAFRALVAQCLVCVPW 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 MPRAPRCRAVRSLLRSHYREVLPLATFVRRLGPQGWRLVQRGDPAAFRALVAQCLVCVPW 60

Qy         61 DARPPPAAPSFRQVSCLKELVARVLQRLCERGAKNVLAFGFALLDGARGGPPEAFTTSVR 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 DARPPPAAPSFRQVSCLKELVARVLQRLCERGAKNVLAFGFALLDGARGGPPEAFTTSVR 120

Qy        121 SYLPNTVTDALRGSGAWGLLLRRVGDDVLVHLLARCALFVLVAPSCAYQVCGPPLYQLGA 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 SYLPNTVTDALRGSGAWGLLLRRVGDDVLVHLLARCALFVLVAPSCAYQVCGPPLYQLGA 180

Qy        181 ATQARPPPHASGPRRRLGCERAWNHSVREAGVPLGLPAPGARRRGGSASRSLPLPKRPRR 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 ATQARPPPHASGPRRRLGCERAWNHSVREAGVPLGLPAPGARRRGGSASRSLPLPKRPRR 240

Qy        241 GAAPEPERTPVGQGSWAHPGRTRGPSDRGFCVVSPARPAEEATSLEGALSGTRHSHPSVG 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 GAAPEPERTPVGQGSWAHPGRTRGPSDRGFCVVSPARPAEEATSLEGALSGTRHSHPSVG 300

Qy        301 RQHHAGPPSTSRPPRPWDTPCPPVYAETKHFLYSSGDKEQLRPSFLLSSLRPSLTGARRL 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 RQHHAGPPSTSRPPRPWDTPCPPVYAETKHFLYSSGDKEQLRPSFLLSSLRPSLTGARRL 360

Qy        361 VETIFLGSRPWMPGTPRRLPRLPQRYWQMRPLFLELLGNHAQCPYGVLLKTHCPLRAAVT 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        361 VETIFLGSRPWMPGTPRRLPRLPQRYWQMRPLFLELLGNHAQCPYGVLLKTHCPLRAAVT 420

Qy        421 PAAGVCAREKPQGSVAAPEEEDTDPRRLVQLLRQHSSPWQVYGFVRACLRRLVPPGLWGS 480
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        421 PAAGVCAREKPQGSVAAPEEEDTDPRRLVQLLRQHSSPWQVYGFVRACLRRLVPPGLWGS 480

Qy        481 RHNERRFLRNTKKFISLGKHAKLSLQELTWKMSVRDCAWLRRSPGVGCVPAAEHRLREEI 540
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        481 RHNERRFLRNTKKFISLGKHAKLSLQELTWKMSVRDCAWLRRSPGVGCVPAAEHRLREEI 540

Qy        541 LAKFLHWLMSVYVVELLRSFFYVTETTFQKNRLFFYRKSVWSKLQSIG 588
              ||||||||||||||||||||||||||||||||||||||||||||||||
Db        541 LAKFLHWLMSVYVVELLRSFFYVTETTFQKNRLFFYRKSVWSKLQSIG 588


RESULT 59
AAY00644
ID   AAY00644 standard; protein; 588 AA.
XX
AC   AAY00644;
XX
DT   26-JUL-1999  (first entry)
XX
DE   N-terminal truncated telomerase (ver. 2) protein sequence.
XX
KW   Telomerase; human; cancer; diagnosis; melanoma; skin cancer; leukaemia;
KW   neuroblastoma; breast carcinoma; colon carcinoma; lymphoma; osteosarcoma;
KW   smooth muscle cell hyperplasia; stem cell proliferation; Wilm's tumour;
KW   stem cell differentiation; organ regeneration; organ differentiation.
XX
OS   Homo sapiens.
OS   Synthetic.
XX
PN   WO9901560-A1.
XX
PD   14-JAN-1999.
XX
PF   01-JUL-1998;   98WO-US013835.
XX
PR   01-JUL-1997;   97US-0051410P.
PR   21-JUL-1997;   97US-0053018P.
PR   21-JUL-1997;   97US-0053329P.
PR   04-AUG-1997;   97US-0054642P.
PR   09-SEP-1997;   97US-0058287P.
XX
PA   (CAMB-) CAMBIA BIOSYSTEMS LLC.
XX
PI   Kilian A,  Bowtell D;
XX
DR   WPI; 1999-106060/09.
DR   N-PSDB; AAX18272.
XX
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```
PT   New isolated vertebrate telomerase genes - used to develop products for
PT   treating cancers or for organ regeneration, nerve cell or brain cell
PT   growth following injury or bone marrow transplantation.
XX
PS   Claim 4; Fig 11t-u; 134pp; English.
XX
CC   This sequence is a truncated human telomerase of the invention. Primers
CC   that amplify the telomerase coding sequence can be used in a method for
CC   diagnosing cancer in a patient. The telomerase can be used for detection,
CC   diagnosis and drug screening. Inhibitors of telomerase activity can be
CC   used to treat cancers such as melanomas, other skin cancers,
CC   neuroblastomas, breast carcinomas, colon carcinomas, leukaemias,
CC   lymphomas, osteosarcomas or smooth muscle cell hyperplasias or skin
CC   growths. Enhancers of telomerase may be used to stimulate stem cell
CC   proliferation and differentiation (expansion of haematopoietic stem cells
CC   could be administered in the bone marrow transplant context). As well,
CC   many tissues have stem cells. Proliferation of these cells may be useful
CC   in wound healing, hair growth, treatment of disease such as Wilm's
CC   tumour, organ regeneration or differentiation after injury or diseases,
CC   nerve cell or brain cell growth following injury. Note: The N-terminus of
CC   this sequence can be replaced by the sequences shown in AAY00656-Y00658
XX
SQ   Sequence 588 AA;

  Query Match             52.7%;  Score 3144;  DB 2;  Length 588;
  Best Local Similarity   99.7%;  Pred. No. 2.2e-255;
  Matches  586;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy          1 MPRAPRCRAVRSLLRSHYREVLPLATFVRRLGPQGWRLVQRGDPAAFRALVAQCLVCVPW 60
              ||||||||||||||||| ||||||||||||||||||||||||||||||||||||||||||
Db          1 MPRAPRCRAVRSLLRSHTREVLPLATFVRRLGPQGWRLVQRGDPAAFRALVAQCLVCVPW 60

Qy         61 DARPPPAAPSFRQVSCLKELVARVLQRLCERGAKNVLAFGFALLDGARGGPPEAFTTSVR 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 DARPPPAAPSFRQVSCLKELVARVLQRLCERGAKNVLAFGFALLDGARGGPPEAFTTSVR 120

Qy        121 SYLPNTVTDALRGSGAWGLLLRRVGDDVLVHLLARCALFVLVAPSCAYQVCGPPLYQLGA 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 SYLPNTVTDALRGSGAWGLLLRRVGDDVLVHLLARCALFVLVAPSCAYQVCGPPLYQLGA 180

Qy        181 ATQARPPPHASGPRRRLGCERAWNHSVREAGVPLGLPAPGARRRGGSASRSLPLPKRPRR 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 ATQARPPPHASGPRRRLGCERAWNHSVREAGVPLGLPAPGARRRGGSASRSLPLPKRPRR 240

Qy        241 GAAPEPERTPVGQGSWAHPGRTRGPSDRGFCVVSPARPAEEATSLEGALSGTRHSHPSVG 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 GAAPEPERTPVGQGSWAHPGRTRGPSDRGFCVVSPARPAEEATSLEGALSGTRHSHPSVG 300

Qy        301 RQHHAGPPSTSRPPRPWDTPCPPVYAETKHFLYSSGDKEQLRPSFLLSSLRPSLTGARRL 360
              ||||||||||||| ||||||||||||||||||||||||||||||||||||||||||||||
Db        301 RQHHAGPPSTSRPPGPWDTPCPPVYAETKHFLYSSGDKEQLRPSFLLSSLRPSLTGARRL 360

Qy        361 VETIFLGSRPWMPGTPRRLPRLPQRYWQMRPLFLELLGNHAQCPYGVLLKTHCPLRAAVT 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        361 VETIFLGSRPWMPGTPRRLPRLPQRYWQMRPLFLELLGNHAQCPYGVLLKTHCPLRAAVT 420

Qy        421 PAAGVCAREKPQGSVAAPEEEDTDPRRLVQLLRQHSSPWQVYGFVRACLRRLVPPGLWGS 480
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        421 PAAGVCAREKPQGSVAAPEEEDTDPRRLVQLLRQHSSPWQVYGFVRACLRRLVPPGLWGS 480

Qy        481 RHNERRFLRNTKKFISLGKHAKLSLQELTWKMSVRDCAWLRRSPGVGCVPAAEHRLREEI 540
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        481 RHNERRFLRNTKKFISLGKHAKLSLQELTWKMSVRDCAWLRRSPGVGCVPAAEHRLREEI 540

Qy        541 LAKFLHWLMSVYVVELLRSFFYVTETTFQKNRLFFYRKSVWSKLQSIG 588
              ||||||||||||||||||||||||||||||||||||||||||||||||
Db        541 LAKFLHWLMSVYVVELLRSFFYVTETTFQKNRLFFYRKSVWSKLQSIG 588


RESULT 60
AAY25463
ID   AAY25463 standard; protein; 622 AA.
XX
AC   AAY25463;
XX
DT   22-SEP-1999  (first entry)
XX
DE   Human CRT-1 protein #3.
XX
KW   CRT-1; reverse transcriptase; telomerase; inhibitor; detection;
KW   telomerase activity; cancer cell; screening; human.
XX
OS   Homo sapiens.
XX
FH   Key             Location/Qualifiers
FT   Protein         1. .622
FT                   /label= CRT-1
FT                   /note= "Partial sequence, no stop codon given"
XX
PN   WO9935261-A1.
XX
PD   15-JUL-1999.
XX
PF   08-JAN-1999;   99WO-JP000039.
XX
PR   08-JAN-1998;   98JP-00013232.
PR   30-JAN-1998;   98JP-00033584.
PR   06-MAY-1998;   98JP-00139177.
XX
PA   (CHUS ) CHUGAI SEIYAKU KK.
XX
PI   Tsuchiya M,  Yoshida K;
XX
DR   WPI; 1999-430393/36.
DR   N-PSDB; AAX88251.
XX
PT   Novel gene, useful in detection of telomerase activity and cancer cells
PT   as well as screening telomerase inhibitors for treatment of cancers.
XX
PS   Example 1; Page 37-39; 44pp; Japanese.
XX
CC   This invention describes novel human CRT-1 genes and their encoded
CC   proteins containing a reverse transcriptase motif, which act as
CC   telomerase inhibitors. The gene, its encoded protein and derived
CC   antibodies can be used to provide base sequence information, detect
CC   telomerase activity and cancer cells, and to screen telomerase
CC   inhibitors. The detection method is simple and effective
XX
SQ   Sequence 622 AA;

  Query Match             52.6%;  Score 3134;  DB 2;  Length 622;
  Best Local Similarity   97.9%;  Pred. No. 1.7e-254;
  Matches  610;  Conservative    3;  Mismatches    6;  Indels    4;  Gaps    1;

Qy        510 WKMSVRDCAWLRRSPGVGCVPAAEHRLREEILAKFLHWLMSVYVVELLRSFFYVTETTFQ 569
              |::: |    |    ||||||||||||||||||||||||||||||||||||||||||||||
Db          4 WRLTRRAVILAR----VGCVPAAEHRLREEILAKFLHWLMSVYVVELLRSFFYVTETTFQ 59

Qy        570 KNRLFFYRKSVWSKLQSIGIRQHLKRVQLRELSEAEVRQHREARPALLTSRLRFIPKPDG 629
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         60 KNRLFFYRKSVWSKLQSIGIRQHLKRVQLRELSEAEVRQHREARPALLTSRLRFIPKPDG 119

Qy        630 LRPIVNMDYVVGARTFRREKRAERLTSRVKALFSVLNYERARRPGLLGASVLGLDDIHRA 689
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        120 LRPIVNMDYVVGARTFRREKRAERLTSRVKALFSVLNYERARRPGLLGASVLGLDDIHRA 179

Qy        690 WRTFVLRVRAQDPPPELYFVKVDVTGAYDTIPQDRLTEVIASIIKPQNTYCVRRYAVVQK 749
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        180 WRTFVLRVRAQDPPPELYFVKVDVTGAYDTIPQDRLTEVIASIIKPQNTYCVRRYAVVQK 239

Qy        750 AAHGHVRKAFKSHVSTLTDLQPYMRQFVAHLQETSPLRDAVVIEQSSSLNEASSGLFDVF 809
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        240 AAHGHVRKAFKSHVSTLTDLQPYMRQFVAHLQETSPLRDAVVIEQSSSLNEASSGLFDVF 299

Qy        810 LRFMCHHAVRIRGKSYVQCQGIPQGSILSTLLCSLCYGDMENKLFAGIRRDGLLLRLVDD 869
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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```
Db        300 LRFMCHHAVRIRGKSYVQCQGIPQGSILSTLLCSLCYGDMENKLFAGIRRDGLLLRLVDD 359

Qy        870 FLLVTPHLTHAKTFLRTLVRGVPEYGCVVNLRKTVVNFPVEDEALGGTAFVQMPAHGLFP 929
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        360 FLLVTPHLTHAKTFLRTLVRGVPEYGCVVNLRKTVVNFPVEDEALGGTAFVQMPAHGLFP 419

Qy        930 WCGLLLDTRTLEVQSDYSSYARTSIRASLTFNRGFKAGRNMRRKLFGVLRLKCHSLFLDL 989
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        420 WCGLLLDTRTLEVQSDYSSYARTSIRASLTFNRGFKAGRNMRRKLFGVLRLKCHSLFLDL 479

Qy        990 QVNSLQTVCTNIYKILLLQAYRFHACVLQLPFHQQVWKNPTFFLRVISDTASLCYSILKA 1049
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        480 QVNSLQTVCTNIYKILLLQAYRFHACVLQLPFHQQVWKNPTFFLRVISDTASLCYSILKA 539

Qy       1050 KNAGMSLGAKGAAGPLPSEAVQWLCHQAFLLKLTRHRVTYVPLLGSLRTAQTQLSRKLPG 1109
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        540 KNAGMSLGAKGAAGPLPSEAVQWLCHQAFLLKLTRHRVTYVPLLGSLRTAQTQLSRKLPG 599

Qy       1110 TTLTALEAAANPALPSDFKTILD 1132
              |||||||||||||||||||||||
Db        600 TTLTALEAAANPALPSDFKTILD 622
```

RESULT 61
AAW97384
ID AAW97384 standard; protein; 591 AA.
XX
AC AAW97384;
XX
DT 14-MAY-1999 (first entry)
XX
DE A catalytic telomerase protein.
XX
KW Catalytic telomerase; diagnosis; disease; telomerase activity.
XX
OS Homo sapiens.
XX
PN JP11046768-A.
XX
PD 23-FEB-1999.
XX
PF 01-AUG-1997; 97JP-00207708.
XX
PR 01-AUG-1997; 97JP-00207708.
XX
PA (MITU) MITSUBISHI CHEM CORP.
XX
DR WPI; 1999-208111/18.
DR N-PSDB; AAX15923.
XX
PT New catalytic protein of telomerase of a higher animal and a gene coding
PT it - useful for diagnosis of diseases caused by the change in activity of
PT a telomerase.
XX
PS Claim 1; Page 11-14; 18pp; Japanese.
XX
CC The present sequence represents a catalytic telomerase protein. The
CC products are useful in drug compositions for the diagnosis of diseases
CC caused by the change in activity of telomerase
XX
SQ Sequence 591 AA;

```
  Query Match           51.1%;  Score 3047;  DB 2;  Length 591;
  Best Local Similarity  100.0%;  Pred. No. 3.3e-247;
  Matches  591;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        542 AKFLHWLMSVYVVELLRSFFYVTETTFQKNRLFFYRKSVWSKLQSIGIRQHLKRVQLREL 601
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 AKFLHWLMSVYVVELLRSFFYVTETTFQKNRLFFYRKSVWSKLQSIGIRQHLKRVQLREL 60

Qy        602 SEAEVRQHREARPALLTSRLRFIPKPDGLRPIVNMDYVVGARTFRREKRAERLTSRVKAL 661
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 SEAEVRQHREARPALLTSRLRFIPKPDGLRPIVNMDYVVGARTFRREKRAERLTSRVKAL 120

Qy        662 FSVLNYERARRPGLLGASVLGLDDIHRAWRTFVLRVRAQDPPPELYFVKVDVTGAYDTIP 721
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 FSVLNYERARRPGLLGASVLGLDDIHRAWRTFVLRVRAQDPPPELYFVKVDVTGAYDTIP 180

Qy        722 QDRLTEVIASIIKPQNTYCVRRYAVVQKAAHGHVRKAFKSHVSTLTDLQPYMRQFVAHLQ 781
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 QDRLTEVIASIIKPQNTYCVRRYAVVQKAAHGHVRKAFKSHVSTLTDLQPYMRQFVAHLQ 240

Qy        782 ETSPLRDAVVIEQSSSLNEASSGLFDVFLRFMCHHAVRIRGKSYVQCQGIPQGSILSTLL 841
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 ETSPLRDAVVIEQSSSLNEASSGLFDVFLRFMCHHAVRIRGKSYVQCQGIPQGSILSTLL 300

Qy        842 CSLCYGDMENKLFAGIRRDGLLLRLVDDFLLVTPHLTHAKTFLRTLVRGVPEYGCVVNLR 901
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 CSLCYGDMENKLFAGIRRDGLLLRLVDDFLLVTPHLTHAKTFLRTLVRGVPEYGCVVNLR 360

Qy        902 KTVVNFPVEDEALGGTAFVQMPAHGLFPWCGLLLDTRTLEVQSDYSSYARTSIRASLTFN 961
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        361 KTVVNFPVEDEALGGTAFVQMPAHGLFPWCGLLLDTRTLEVQSDYSSYARTSIRASLTFN 420

Qy        962 RGFKAGRNMRRKLFGVLRLKCHSLFLDLQVNSLQTVCTNIYKILLLQAYRFHACVLQLPF 1021
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        421 RGFKAGRNMRRKLFGVLRLKCHSLFLDLQVNSLQTVCTNIYKILLLQAYRFHACVLQLPF 480

Qy       1022 HQQVWKNPTFFLRVISDTASLCYSILKAKNAGMSLGAKGAAGPLPSEAVQWLCHQAFLLK 1081
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        481 HQQVWKNPTFFLRVISDTASLCYSILKAKNAGMSLGAKGAAGPLPSEAVQWLCHQAFLLK 540

Qy       1082 LTRHRVTYVPLLGSLRTAQTQLSRKLPGTTLTALEAAANPALPSDFKTILD 1132
              ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        541 LTRHRVTYVPLLGSLRTAQTQLSRKLPGTTLTALEAAANPALPSDFKTILD 591
```

RESULT 62
AAO29840
ID AAO29840 standard; protein; 500 AA.
XX
AC AAO29840;
XX
DT 27-AUG-2003 (first entry)
XX
DE Human telomerase reverse transcriptase (hTRT).
XX
KW Human; telomerase reverse transcriptase; MHC; tumour-associated antigen;
KW hyperproliferative disease; major histocompatibility complex; hTRT; TAA;
KW immune-mediated disease; systemic lupus erythematosus; protein therapy;
KW Grave's disease; multiple sclerosis; atherosclerosis; cancer; diabetes;
KW Crohn's disease; gene therapy; arthritis; enzyme; vaccine; vasculitis;
KW cell therapy.
XX
OS Homo sapiens.
XX
PN WO2003038047-A2.
XX
PD 08-MAY-2003.
XX
PF 29-OCT-2002; 2002WO-US034588.
XX
PR 29-OCT-2001; 2001US-0345012P.
XX
PA (BAYU) BAYLOR COLLEGE MEDICINE.
XX
PI Chen S, Zhaoyang Y, Schroers R;
XX
DR WPI; 2003-430511/40.
XX
PT New human telomerase reverse transcriptase tumor-associated MHC-I or MHC-
PT II restricted polynucleotides and antigens, useful for treating cancers
PT (e.g. lung or bone cancer or lymphomas), Crohn's disease or multiple
PT sclerosis.
XX
PS Example 9; Fig 2C; 143pp; English.

```
XX
CC   The invention relates to human telomerase reverse transcriptase (hTRT)
CC   major histocompatibility complex (MHC)-I and MHC-II restricted tumour-
CC   associated antigens (TAA) and polynucleotides encoding such proteins. The
CC   invention is useful for treating hyperproliferative diseases such as
CC   cancer (e.g. lung cancer, head and neck cancer, pancreatic cancer, breast
CC   cancer, prostate cancer, renal cancer, bone cancer, testicular cancer,
CC   cervical cancer, gastrointestinal cancer, lymphomas, colon cancer, pre-
CC   neoplastic lesions in the lung, melanoma or bladder cancer) or immune-
CC   mediated diseases which include arthritis, Crohn's disease, vasculitis,
CC   Grave's disease, multiple sclerosis, atherosclerosis, diabetes, systemic
CC   lupus erythematosus etc. The invention is used in gene therapy, protein
CC   therapy, cell therapy and also in the preparation of vaccines. The
CC   present sequence is hTRT protein
XX
SQ   Sequence 500 AA;

  Query Match             43.4%;  Score 2590;  DB 6;  Length 500;
  Best Local Similarity   100.0%;  Pred. No. 7.8e-209;
  Matches  500;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        533 EHRLREEILAKFLHWLMSVYVVELLRSFFYVTETTFQKNRLFFYRKSVWSKLQSIGIRQH 592
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 EHRLREEILAKFLHWLMSVYVVELLRSFFYVTETTFQKNRLFFYRKSVWSKLQSIGIRQH 60

Qy        593 LKRVQLRELSEAEVRQHREARPALLTSRLRFIPKPDGLRPIVNMDYVVGARTFRREKRAE 652
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 LKRVQLRELSEAEVRQHREARPALLTSRLRFIPKPDGLRPIVNMDYVVGARTFRREKRAE 120

Qy        653 RLTSRVKALFSVLNYERARRPGLLGASVLGLDDIHRAWRTFVLRVRAQDPPPELYFVKVD 712
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 RLTSRVKALFSVLNYERARRPGLLGASVLGLDDIHRAWRTFVLRVRAQDPPPELYFVKVD 180

Qy        713 VTGAYDTIPQDRLTEVIASIIKPQNTYCVRRYAVVQKAAHGHVRKAFKSHVSTLTDLQPY 772
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 VTGAYDTIPQDRLTEVIASIIKPQNTYCVRRYAVVQKAAHGHVRKAFKSHVSTLTDLQPY 240

Qy        773 MRQFVAHLQETSPLRDAVVIEQSSSLNEASSGLFDVFLRFMCHHAVRIRGKSYVQCQGIP 832
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 MRQFVAHLQETSPLRDAVVIEQSSSLNEASSGLFDVFLRFMCHHAVRIRGKSYVQCQGIP 300

Qy        833 QGSILSTLLCSLCYGDMENKLFAGIRRDGLLLRLVDDFLLVTPHLTHAKTFLRTLVRGVP 892
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 QGSILSTLLCSLCYGDMENKLFAGIRRDGLLLRLVDDFLLVTPHLTHAKTFLRTLVRGVP 360

Qy        893 EYGCVVNLRKTVVNFPVEDEALGGTAFVQMPAHGLFPWCGLLLDTRTLEVQSDYSSYART 952
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        361 EYGCVVNLRKTVVNFPVEDEALGGTAFVQMPAHGLFPWCGLLLDTRTLEVQSDYSSYART 420

Qy        953 SIRASLTFNRGFKAGRNMRRKLFGVLRLKCHSLFLDLQVNSLQTVCTNIYKILLLQAYRF 1012
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        421 SIRASLTFNRGFKAGRNMRRKLFGVLRLKCHSLFLDLQVNSLQTVCTNIYKILLLQAYRF 480

Qy       1013 HACVLQLPFHQQVWKNPTFF 1032
              ||||||||||||||||||||
Db        481 HACVLQLPFHQQVWKNPTFF 500


RESULT 63
ABB99678
ID   ABB99678 standard; protein; 499 AA.
XX
AC   ABB99678;
XX
DT   28-MAR-2003  (first entry)
XX
DE   Amino acid sequence of human telomerase reverse transcriptase fragment.
XX
KW   Human; telomerase reverse transcriptase; hTERT; T cell response; vaccine;
KW   cancer.
XX
OS   Homo sapiens.
XX
PN   WO200294312-A1.
XX
PD   28-NOV-2002.
XX
PF   16-MAY-2002; 2002WO-NO000176.
XX
PR   21-MAY-2001; 2001GB-00012342.
XX
PA   (GEMV-) GEMVAX AS.
XX
PI   Eriksen JA,  Gaudernack G,  Moller M,  Saeboe-Larssen S;
XX
DR   WPI; 2003-129380/12.
XX
PT   New polypeptides derived from human telomerase reverse transcriptase,
PT   useful in preparing a medicament for treating or preventing cancer, or in
PT   preparing a diagnostic for diagnosing cancer, e.g. breast cancer or
PT   prostate cancer.
XX
PS   Disclosure; Fig 2; 56pp; English.
XX
CC   The present sequence represents a fragment of human telomerase reverse
CC   transcriptase (hTERT). The specification describes peptides derived from
CC   hTERT, which are capable of inducing a T cell response and are used in
CC   medicine. The hTERT peptides and nucleic acids encoding them are useful
CC   in preparing a medicament, which is a vaccine, an antisense molecule, or
CC   is capable of generating an antisense molecule in vivo, for treating
CC   cancer, or in preparing a diagnostic for diagnosing cancer. The cancer
CC   is, for example, breast cancer, prostate cancer, pancreatic cancer, colo-
CC   rectal cancer, lung cancer, malignant melanoma, leukemia, lymphoma,
CC   ovarian cancer, cervical cancer, or a biliary tract carcinoma
XX
SQ   Sequence 499 AA;

  Query Match             43.2%;  Score 2576;  DB 6;  Length 499;
  Best Local Similarity   100.0%;  Pred. No. 1.2e-207;
  Matches  499;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        634 VNMDYVVGARTFRREKRAERLTSRVKALFSVLNYERARRPGLLGASVLGLDDIHRAWRTF 693
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 VNMDYVVGARTFRREKRAERLTSRVKALFSVLNYERARRPGLLGASVLGLDDIHRAWRTF 60

Qy        694 VLRVRAQDPPPELYFVKVDVTGAYDTIPQDRLTEVIASIIKPQNTYCVRRYAVVQKAAHG 753
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 VLRVRAQDPPPELYFVKVDVTGAYDTIPQDRLTEVIASIIKPQNTYCVRRYAVVQKAAHG 120

Qy        754 HVRKAFKSHVSTLTDLQPYMRQFVAHLQETSPLRDAVVIEQSSSLNEASSGLFDVFLRFM 813
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 HVRKAFKSHVSTLTDLQPYMRQFVAHLQETSPLRDAVVIEQSSSLNEASSGLFDVFLRFM 180

Qy        814 CHHAVRIRGKSYVQCQGIPQGSILSTLLCSLCYGDMENKLFAGIRRDGLLLRLVDDFLLV 873
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 CHHAVRIRGKSYVQCQGIPQGSILSTLLCSLCYGDMENKLFAGIRRDGLLLRLVDDFLLV 240

Qy        874 TPHLTHAKTFLRTLVRGVPEYGCVVNLRKTVVNFPVEDEALGGTAFVQMPAHGLFPWCGL 933
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 TPHLTHAKTFLRTLVRGVPEYGCVVNLRKTVVNFPVEDEALGGTAFVQMPAHGLFPWCGL 300

Qy        934 LLDTRTLEVQSDYSSYARTSIRASLTFNRGFKAGRNMRRKLFGVLRLKCHSLFLDLQVNS 993
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 LLDTRTLEVQSDYSSYARTSIRASLTFNRGFKAGRNMRRKLFGVLRLKCHSLFLDLQVNS 360

Qy        994 LQTVCTNIYKILLLQAYRFHACVLQLPFHQQVWKNPTFFLRVISDTASLCYSILKAKNAG 1053
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        361 LQTVCTNIYKILLLQAYRFHACVLQLPFHQQVWKNPTFFLRVISDTASLCYSILKAKNAG 420

Qy       1054 MSLGAKGAAGPLPSEAVQWLCHQAFLLKLTRHRVTYVPLLGSLRTAQTQLSRKLPGTTLT 1113
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        421 MSLGAKGAAGPLPSEAVQWLCHQAFLLKLTRHRVTYVPLLGSLRTAQTQLSRKLPGTTLT 480

Qy       1114 ALEAAANPALPSDFKTILD 1132
              |||||||||||||||||||
Db        481 ALEAAANPALPSDFKTILD 499
```

RESULT 64
ADD21415
ID ADD21415 standard; protein; 1131 AA.
XX
AC ADD21415;
XX
DT 15-JAN-2004 (first entry)
XX
DE Frog TERT protein related to continual cell growth.
XX
KW continual growth; cultured cell; cyclin dependent kinase; cdk4; cdk2;
KW cdk6; activating mutation; cell growth; cell division; cell cycle;
KW cancer-causing agent; continual growth-induced cell; enzyme; TERT;
KW telomerase; frog.
XX
OS Xenopus laevis.
XX
PN WO2003044169-A2.
XX
PD 30-MAY-2003.
XX
PF 15-NOV-2002; 2002WO-US036729.
XX
PR 15-NOV-2001; 2001US-0334760P.
XX
PA (UTEM) UNIV TEMPLE.
XX
PI Reddy PE, Rane SG, Mettus RV;
XX
DR WPI; 2003-449813/42.
XX
PT A composition for reversibly inducing continual growth in normal cells
PT comprises a cyclin dependent kinase protein (e.g. cdk4, cdk2 or cdk6) or
PT its active fragment, derivative, homolog or analog, having an activating
PT mutation.
XX
PS Claim 12; Page 116-119; 77pp; English.
XX
CC This invention relates to a novel composition for inducing a reversible
CC state of a continual growth in cultured cells and comprises at least one
CC compound comprising a cyclin dependent kinase (cdk)4, cdk2 or cdk6
CC protein having an activating mutation. Growth and division of living
CC cells involve a regular series of events and processes that comprise the
CC cell cycle. Cyclin dependent kinases cdk2, cdk4 and cdk6 are involved in
CC the control of G1, the point at which cells irrevocably commit to DNA
CC synthesis and thus enter the cell cycle. The invention is useful in
CC reversibly inducing continual growth in normal cells and may allow the
CC screening of cancer-causing agents with the continual growth-induced
CC cells. The present sequence is that of the frog TERT protein, the
CC catalytic subunit of telomerase, related to the invention. Note: Due to
CC an error in the specification or sequence listing, the Seq ID numbers
CC given in the disclosure do not correspond to those given in the sequence
CC listing. It is therefore unclear which Seq ID number corresponds to which
CC sequence and exactly which sequence is being claimed.
XX
SQ Sequence 1131 AA;

Query Match 37.9%; Score 2260; DB 7; Length 1131;
Best Local Similarity 43.0%; Pred. No. 1.5e-180;
Matches 500; Conservative 189; Mismatches 354; Indels 120; Gaps 23;

RESULT 65
AAY25462

```
ID   AAY25462 standard; protein; 438 AA.
XX
AC   AAY25462;
XX
DT   22-SEP-1999  (first entry)
XX
DE   Human CRT-1 protein #2.
XX
KW   CRT-1; reverse transcriptase; telomerase; inhibitor; detection;
KW   telomerase activity; cancer cell; screening; human.
XX
OS   Homo sapiens.
XX
FH   Key             Location/Qualifiers
FT   Protein         1. .438
FT                   /label= CRT-1
FT                   /note= "Partial sequence, no stop codon given"
XX
PN   WO9935261-A1.
XX
PD   15-JUL-1999.
XX
PF   08-JAN-1999;   99WO-JP000039.
XX
PR   08-JAN-1998;   98JP-00013232.
PR   30-JAN-1998;   98JP-00033584.
PR   06-MAY-1998;   98JP-00139177.
XX
PA   (CHUS ) CHUGAI SEIYAKU KK.
XX
PI   Tsuchiya M,  Yoshida K;
XX
DR   WPI; 1999-430393/36.
DR   N-PSDB; AAX88250.
XX
PT   Novel gene, useful in detection of telomerase activity and cancer cells
PT   as well as screening telomerase inhibitors for treatment of cancers.
XX
PS   Example 1; Page 35-36; 44pp; Japanese.
XX
CC   This invention describes novel human CRT-1 genes and their encoded
CC   proteins containing a reverse transcriptase motif, which act as
CC   telomerase inhibitors. The gene, its encoded protein and derived
CC   antibodies can be used to provide base sequence information, detect
CC   telomerase activity and cancer cells, and to screen telomerase
CC   inhibitors. The detection method is simple and effective
XX
SQ   Sequence 438 AA;

  Query Match             36.6%;  Score 2184;  DB 2;  Length 438;
  Best Local Similarity   97.0%;  Pred. No. 9.8e-175;
  Matches  425;  Conservative    3;  Mismatches    6;  Indels    4;  Gaps    1;

Qy        510 WKMSVRDCAWLRRSPGVGCVPAAEHRLREEILAKFLHWLMSVYVVELLRSFFYVTETTFQ 569
              |::: |    |    |||||||||||||||||||||||||||||||||||||||||||||
Db          4 WRLTRRAVILAR----VGCVPAAEHRLREEILAKFLHWLMSVYVVELLRSFFYVTETTFQ 59

Qy        570 KNRLFFYRKSVWSKLQSIGIRQHLKRVQLRELSEAEVRQHREARPALLTSRLRFIPKPDG 629
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         60 KNRLFFYRKSVWSKLQSIGIRQHLKRVQLRELSEAEVRQHREARPALLTSRLRFIPKPDG 119

Qy        630 LRPIVNMDYVVGARTFRREKRAERLTSRVKALFSVLNYERARRPGLLGASVLGLDDIHRA 689
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        120 LRPIVNMDYVVGARTFRREKRAERLTSRVKALFSVLNYERARRPGLLGASVLGLDDIHRA 179

Qy        690 WRTFVLRVRAQDPPPELYFVKVDVTGAYDTIPQDRLTEVIASIIKPQNTYCVRRYAVVQK 749
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        180 WRTFVLRVRAQDPPPELYFVKVDVTGAYDTIPQDRLTEVIASIIKPQNTYCVRRYAVVQK 239

Qy        750 AAHGHVRKAFKSHVSTLTDLQPYMRQFVAHLQETSPLRDAVVIEQSSSLNEASSGLFDVF 809
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        240 AAHGHVRKAFKSHVSTLTDLQPYMRQFVAHLQETSPLRDAVVIEQSSSLNEASSGLFDVF 299

Qy        810 LRFMCHHAVRIRGKSYVQCQGIPQGSILSTLLCSLCYGDMENKLFAGIRRDGLLLRLVDD 869
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        300 LRFMCHHAVRIRGKSYVQCQGIPQGSILSTLLCSLCYGDMENKLFAGIRRDGLLLRLVDD 359

Qy        870 FLLVTPHLTHAKTFLRTLVRGVPEYGCVVNLRKTVVNFPVEDEALGGTAFVQMPAHGLFP 929
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        360 FLLVTPHLTHAKTFLRTLVRGVPEYGCVVNLRKTVVNFPVEDEALGGTAFVQMPAHGLFP 419

Qy        930 WCGLLLDTRTLEVQSDYS 947
              ||||||||||||||||||
Db        420 WCGLLLDTRTLEVQSDYS 437


RESULT 66
ABB99680
ID   ABB99680 standard; protein; 436 AA.
XX
AC   ABB99680;
XX
DT   28-MAR-2003  (first entry)
XX
DE   Splice variant of a human telomerase reverse transcriptase fragment.
XX
KW   Human; telomerase reverse transcriptase; hTERT; T cell response; vaccine;
KW   cancer.
XX
OS   Homo sapiens.
XX
PN   WO200294312-A1.
XX
PD   28-NOV-2002.
XX
PF   16-MAY-2002; 2002WO-NO000176.
XX
PR   21-MAY-2001; 2001GB-00012342.
XX
PA   (GEMV-) GEMVAX AS.
XX
PI   Eriksen JA,  Gaudernack G,  Moller M,  Saeboe-Larssen S;
XX
DR   WPI; 2003-129380/12.
XX
PT   New polypeptides derived from human telomerase reverse transcriptase,
PT   useful in preparing a medicament for treating or preventing cancer, or in
PT   preparing a diagnostic for diagnosing cancer, e.g. breast cancer or
PT   prostate cancer.
XX
PS   Disclosure; Fig 2; 56pp; English.
XX
CC   The present sequence represents a splice variant of a fragment of human
CC   telomerase reverse transcriptase (hTERT). The specification describes
CC   peptides derived from hTERT, which are capable of inducing a T cell
CC   response and are used in medicine. The hTERT peptides and nucleic acids
CC   encoding them are useful in preparing a medicament, which is a vaccine,
CC   an antisense molecule, or is capable of generating an antisense molecule
CC   in vivo, for treating cancer, or in preparing a diagnostic for diagnosing
CC   cancer. The cancer is, for example, breast cancer, prostate cancer,
CC   pancreatic cancer, colo-rectal cancer, lung cancer, malignant melanoma,
CC   leukemia, lymphoma, ovarian cancer, cervical cancer, or a biliary tract
CC   carcinoma
XX
SQ   Sequence 436 AA;

  Query Match             36.6%;  Score 2181;  DB 6;  Length 436;
  Best Local Similarity   100.0%;  Pred. No. 1.8e-174;
  Matches  421;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        634 VNMDYVVGARTFRREKRAERLTSRVKALFSVLNYERARRPGLLGASVLGLDDIHRAWRTF 693
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 VNMDYVVGARTFRREKRAERLTSRVKALFSVLNYERARRPGLLGASVLGLDDIHRAWRTF 60

Qy        694 VLRVRAQDPPPELYFVKVDVTGAYDTIPQDRLTEVIASIIKPQNTYCVRRYAVVQKAAHG 753
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
```

```
Db         61 VLRVRAQDPPPELYFVKVDVTGAYDTIPQDRLTEVIASIIKPQNTYCVRRYAVVQKAAHG 120

Qy        754 HVRKAFKSHVSTLTDLQPYMRQFVAHLQETSPLRDAVVIEQSSSLNEASSGLFDVFLRFM 813
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 HVRKAFKSHVSTLTDLQPYMRQFVAHLQETSPLRDAVVIEQSSSLNEASSGLFDVFLRFM 180

Qy        814 CHHAVRIRGKSYVQCQGIPQGSILSTLLCSLCYGDMENKLFAGIRRDGLLLRLVDDFLLV 873
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 CHHAVRIRGKSYVQCQGIPQGSILSTLLCSLCYGDMENKLFAGIRRDGLLLRLVDDFLLV 240

Qy        874 TPHLTHAKTFLRTLVRGVPEYGCVVNLRKTVVNFPVEDEALGGTAFVQMPAHGLFPWCGL 933
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 TPHLTHAKTFLRTLVRGVPEYGCVVNLRKTVVNFPVEDEALGGTAFVQMPAHGLFPWCGL 300

Qy        934 LLDTRTLEVQSDYSSYARTSIRASLTFNRGFKAGRNMRRKLFGVLRLKCHSLFLDLQVNS 993
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 LLDTRTLEVQSDYSSYARTSIRASLTFNRGFKAGRNMRRKLFGVLRLKCHSLFLDLQVNS 360

Qy        994 LQTVCTNIYKILLLQAYRFHACVLQLPFHQQVWKNPTFFLRVISDTASLCYSILKAKNAG 1053
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        361 LQTVCTNIYKILLLQAYRFHACVLQLPFHQQVWKNPTFFLRVISDTASLCYSILKAKNAG 420

Qy       1054 M 1054
              |
Db        421 M 421
```

```
RESULT 67
ABB99679
ID   ABB99679 standard; protein; 463 AA.
XX
AC   ABB99679;
XX
DT   28-MAR-2003  (first entry)
XX
DE   Splice variant of a human telomerase reverse transcriptase fragment.
XX
KW   Human; telomerase reverse transcriptase; hTERT; T cell response; vaccine;
KW   cancer.
XX
OS   Homo sapiens.
XX
PN   WO200294312-A1.
XX
PD   28-NOV-2002.
XX
PF   16-MAY-2002; 2002WO-NO000176.
XX
PR   21-MAY-2001; 2001GB-00012342.
XX
PA   (GEMV-) GEMVAX AS.
XX
PI   Eriksen JA,  Gaudernack G,  Moller M,  Saeboe-Larssen S;
XX
DR   WPI; 2003-129380/12.
XX
PT   New polypeptides derived from human telomerase reverse transcriptase,
PT   useful in preparing a medicament for treating or preventing cancer, or in
PT   preparing a diagnostic for diagnosing cancer, e.g. breast cancer or
PT   prostate cancer.
XX
PS   Disclosure; Fig 2; 56pp; English.
XX
CC   The present sequence represents a splice variant of a fragment of human
CC   telomerase reverse transcriptase (hTERT). The specification describes
CC   peptides derived from hTERT, which are capable of inducing a T cell
CC   response and are used in medicine. The hTERT peptides and nucleic acids
CC   encoding them are useful in preparing a medicament, which is a vaccine,
CC   an antisense molecule, or is capable of generating an antisense molecule
CC   in vivo, for treating cancer, or in preparing a diagnostic for diagnosing
CC   cancer. The cancer is, for example, breast cancer, prostate cancer,
CC   pancreatic cancer, colo-rectal cancer, lung cancer, malignant melanoma,
CC   leukemia, lymphoma, ovarian cancer, cervical cancer, or a biliary tract
CC   carcinoma
XX
SQ   Sequence 463 AA;

  Query Match             36.4%;  Score 2170;  DB 6;  Length 463;
  Best Local Similarity   100.0%;  Pred. No. 1.6e-173;
  Matches  419;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        634 VNMDYVVGARTFRREKRAERLTSRVKALFSVLNYERARRPGLLGASVLGLDDIHRAWRTF 693
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 VNMDYVVGARTFRREKRAERLTSRVKALFSVLNYERARRPGLLGASVLGLDDIHRAWRTF 60

Qy        694 VLRVRAQDPPPELYFVKVDVTGAYDTIPQDRLTEVIASIIKPQNTYCVRRYAVVQKAAHG 753
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 VLRVRAQDPPPELYFVKVDVTGAYDTIPQDRLTEVIASIIKPQNTYCVRRYAVVQKAAHG 120

Qy        754 HVRKAFKSHVSTLTDLQPYMRQFVAHLQETSPLRDAVVIEQSSSLNEASSGLFDVFLRFM 813
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 HVRKAFKSHVSTLTDLQPYMRQFVAHLQETSPLRDAVVIEQSSSLNEASSGLFDVFLRFM 180

Qy        814 CHHAVRIRGKSYVQCQGIPQGSILSTLLCSLCYGDMENKLFAGIRRDGLLLRLVDDFLLV 873
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 CHHAVRIRGKSYVQCQGIPQGSILSTLLCSLCYGDMENKLFAGIRRDGLLLRLVDDFLLV 240

Qy        874 TPHLTHAKTFLRTLVRGVPEYGCVVNLRKTVVNFPVEDEALGGTAFVQMPAHGLFPWCGL 933
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 TPHLTHAKTFLRTLVRGVPEYGCVVNLRKTVVNFPVEDEALGGTAFVQMPAHGLFPWCGL 300

Qy        934 LLDTRTLEVQSDYSSYARTSIRASLTFNRGFKAGRNMRRKLFGVLRLKCHSLFLDLQVNS 993
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 LLDTRTLEVQSDYSSYARTSIRASLTFNRGFKAGRNMRRKLFGVLRLKCHSLFLDLQVNS 360

Qy        994 LQTVCTNIYKILLLQAYRFHACVLQLPFHQQVWKNPTFFLRVISDTASLCYSILKAKNA 1052
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        361 LQTVCTNIYKILLLQAYRFHACVLQLPFHQQVWKNPTFFLRVISDTASLCYSILKAKNA 419
```

```
RESULT 68
AAY25461
ID   AAY25461 standard; protein; 437 AA.
XX
AC   AAY25461;
XX
DT   22-SEP-1999  (first entry)
XX
DE   Human CRT-1 protein #1.
XX
KW   CRT-1; reverse transcriptase; telomerase; inhibitor; detection;
KW   telomerase activity; cancer cell; screening; human.
XX
OS   Homo sapiens.
XX
FH   Key             Location/Qualifiers
FT   Protein         1. .437
FT                   /label= CRT-1
FT                   /note= "Partial sequence, no stop codon given"
XX
PN   WO9935261-A1.
XX
PD   15-JUL-1999.
XX
PF   08-JAN-1999;   99WO-JP000039.
XX
PR   08-JAN-1998;   98JP-00013232.
PR   30-JAN-1998;   98JP-00033584.
PR   06-MAY-1998;   98JP-00139177.
XX
PA   (CHUS ) CHUGAI SEIYAKU KK.
XX
PI   Tsuchiya M,  Yoshida K;
XX
DR   WPI; 1999-430393/36.
DR   N-PSDB; AAX88243.
```

```
XX
PT   Novel gene, useful in detection of telomerase activity and cancer cells
PT   as well as screening telomerase inhibitors for treatment of cancers.
XX
PS   Claim 2; Page 31-32; 44pp; Japanese.
XX
CC   This invention describes novel human CRT-1 genes and their encoded
CC   proteins containing a reverse transcriptase motif, which act as
CC   telomerase inhibitors. The gene, its encoded protein and derived
CC   antibodies can be used to provide base sequence information, detect
CC   telomerase activity and cancer cells, and to screen telomerase
CC   inhibitors. The detection method is simple and effective
XX
SQ   Sequence 437 AA;

  Query Match             36.4%;  Score 2169.5;  DB 2;  Length 437;
  Best Local Similarity   96.8%;  Pred. No. 1.6e-173;
  Matches  424;  Conservative    3;  Mismatches    6;  Indels    5;  Gaps    2;

Qy        510 WKMSVRDCAWLRRSPGVGCVPAAEHRLREEILAKFLHWLMSVYVVELLRSFFYVTETTFQ 569
              |::: |     |    ||||||||||||||||||||||||||||||||||||||||||||
Db          4 WRLTRRAVILAR----VGCVPAAEHRLREEILAKFLHWLMSVYVVELLRSFFYVTETTFQ 59

Qy        570 KNRLFFYRKSVWSKLQSIGIRQHLKRVQLRELSEAEVRQHREARPALLTSRLRFIPKPDG 629
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         60 KNRLFFYRKSVWSKLQSIGIRQHLKRVQLRELSEAEVRQHREARPALLTSRLRFIPKPDG 119

Qy        630 LRPIVNMDYVVGARTFRREKRAERLTSRVKALFSVLNYERARRPGLLGASVLGLDDIHRA 689
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        120 LRPIVNMDYVVGARTFRREKRAERLTSRVKALFSVLNYERARRPGLLGASVLGLDDIHRA 179

Qy        690 WRTFVLRVRAQDPPPELYFVKVDVTGAYDTIPQDRLTEVIASIIKPQNTYCVRRYAVVQK 749
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        180 WRTFVLRVRAQDPPPELYFVKVDVTGAYDTIPQDRLTEVIASIIKPQNTYCVRRYAVVQK 239

Qy        750 AAHGHVRKAFKSHVSTLTDLQPYMRQFVAHLQETSPLRDAVVIEQSSSLNEASSGLFDVF 809
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        240 AAHGHVRKAFKSHVSTLTDLQPYMRQFVAHLQETSPLRDAVVIEQSSSLNEASSGLFDVF 299

Qy        810 LRFMCHHAVRIRGKSYVQCQGIPQGSILSTLLCSLCYGDMENKLFAGIRRDGLLLRLVDD 869
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        300 LRFMCHHAVRIRGKSYVQCQGIPQGSILSTLLCSLCYGDMENKLFAGIRRDGLLLRLVDD 359

Qy        870 FLLVTPHLTHAKTFLRTLVRGVPEYGCVVNLRKTVVNFPVEDEALGGTAFVQMPAHGLFP 929
              | ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        360 F-LVTPHLTHAKTFLRTLVRGVPEYGCVVNLRKTVVNFPVEDEALGGTAFVQMPAHGLFP 418

Qy        930 WCGLLLDTRTLEVQSDYS 947
              ||||||||||||||||||
Db        419 WCGLLLDTRTLEVQSDYS 436


RESULT 69
ADG90607
ID   ADG90607 standard; protein; 743 AA.
XX
AC   ADG90607;
XX
DT   25-MAR-2004  (first entry)
XX
DE   Dog TERT SEQ ID NO:10.
XX
KW   dog; immune response; telomerase reverse transcriptase; TERT; cytostatic;
KW   immunostimulant; cancer; cytotoxic T cell response.
XX
OS   Canis familiaris.
XX
PN   WO2004002408-A2.
XX
PD   08-JAN-2004.
XX
PF   24-JUN-2003; 2003WO-US019844.
XX
PR   27-JUN-2002; 2002US-0393295P.
XX
PA   (GERO-) GERON CORP.
XX
PI   Majumdar A,  Ferber IA,  Frolkis M,  Wang Z;
XX
DR   WPI; 2004-071946/07.
DR   N-PSDB; ADG90606.
XX
PT   Eliciting an immune response in a mammal specific for its own telomerase
PT   reverse transcriptase (TERT), useful for treating or preventing cancer,
PT   comprises administering a composition containing TERT of another
PT   mammalian species.
XX
PS   Claim 10; SEQ ID NO 10; 44pp; English.
XX
CC   The invention relates to a novel method for eliciting an immune response
CC   in a mammalian subject that is specific for its own telomerase reverse
CC   transcriptase (TERT), comprising administering an immunogenic composition
CC   containing a protein with at least 20 consecutive amino acids of TERT of
CC   another mammalian species, or a nucleic acid encoding the protein. A
CC   composition of the invention has cytostatic, and immunostimulant
CC   activity. The protein or the nucleic acid encoding the protein is useful
CC   in the manufacture of a medicament for the treatment of cancer in a human
CC   or for eliciting a cytotoxic T cell response in a human.
XX
SQ   Sequence 743 AA;

  Query Match             36.3%;  Score 2166.5;  DB 8;  Length 743;
  Best Local Similarity   56.7%;  Pred. No. 6.2e-173;
  Matches  467;  Conservative   63;  Mismatches  151;  Indels  143;  Gaps   20;

Qy          1 MPRAPRCRAVRSLLRSHYREVLPLATFVRRLGPQGWRLVQRGDPAAFRALVAQCLVCVPW 60
              ||||||||||:|||  ||||||||||:||||| |  ||:||||||||||||||||||||
Db          1 MPRAPRCRAVRALLRGRYREVLPLATFLRRLGPPGRLLVRRGDPAAFRALVAQCLVCVPW 60

Qy         61 DARPPPAAPSFRQVSCLKELVARVLQRLCERGAKNVLAFGFALLDGARGGPPEAFTTSVR 120
              ||||||||  |||                          ||||||||||||||| |||||||
Db         61 GARPPPAAPCFRQ----------------------LAFGFALLDGARGGPPVAFTTSVR 97

Qy        121 SYLPNTVTDALRGSGAWGLLLRRVGDDVLVHLLARCALFVLVAPSCAYQVCGPPLYQLGA 180
              ||||||||: |||||||||||||||||| ||||||||::|||||||||||||||     :
Db         98 SYLPNTVTETLRGSGAWGLLLRRVGDDVLTHLLARCALYLLVAPSCAYQVCGPP-----S 152

Qy        181 ATQARPPPHASGPRRRLGCERAWNHSVREAGVPLGLPAPGARRRGGSASRSLPLPKRPRR 240
              | | ||   | ||                        |||| :  |      :     || |
Db        153 TTSAPPPLCRSRPRS------------------PLPAPRSAGRARDLRPTRQARTRPAR 193

Qy        241 GAAPEPERTPVGQGSWAHPGRTRGPSDRGFCVVSPARPAEEATSLEGALSGTRHSHPSVG 300
              |:   |||:       |    | | ||              :||:   :   |  : | :
Db        194 GS---PERSSGSASQWRSRRRHR-PS-------------QATAPVASRVYTCRALPQLA 235

Qy        301 RQHHAGPPSTSR------PPRPWDTPCPPVYAETKHFLYSSGDKEQLRPSFLLSSLRPSL 354
              :   ||| :|        | |   |  | : ||| ||| || :|:|||||||:| |:|
Db        236 WE--GGPPDSSNHPSLDTSPGPQGVPHDPAHPETKRFLYCSGGRERLRPSFLLSALPPTL 293

Qy        355 TGARRLVETIFLGSRPWMPGTPRRLPRLPQRYWQMRPLFLELLGNHAQCPYGVLLKTHCP 414
              |||:|||||||| |  ||  ||: ||| |||:||||| |||||||:|||  ||:||||
Db        294 -GARKLVETIFLGSAPQKPGAARRMRRLPARYWRMRPLFQELLGNHARCPYRALLRTHCP 352

Qy        415 LRAAVTP---------AAGVCAREKPQGSVAAPEEEDTDPRRLVQLLRQHSSPWQVYGFV 465
              |||               |:|  |:|   ||||:|: ||  |||||||||||||| |:
Db        353 LRAMAAKEGSGNQAHRGVGICPLERP---VAAPQEQ-TDSTRLVQLLRQHSSPWQVYAFL 408

Qy        466 RACLRRLVPPGLWGSRHNERRFLRNTKKFISLGKHAKLSLQELTWKMSVRDCAWLRRSPG 525
              ||||  ||| |||||||:|||||| ||||||||||||||||||| |||| ||  :||
Db        409 RACLCWLVPTGLWGSRHNQRRFLRNVKKFISLGKHAKLSLQELTWKMKVRDCTWLHGNPG 468

Qy        526 VGC----------------------VP---AAEHRLREEILAKFLHWLMSVYVVELLRSF 560
              |                       :|    :||         || |  |       | :
Db        469 EECRVSRCLVGLQEGPGSQPECGRPLPPNHPSEH--------PFLCWAGS-DCPACLSAP 519

Qy        561 FYVTETTFQKNRL-----------FFYRKSVWSKLQS---------IGIRQHL-KRVQLR 599
```

```
Db        520 RLPSQTSPHPQRLPGCPHLLPGVMRHHEMSSWWRPSSPYPGHTWLLIGCAPQLFNSVHLR 579

Qy        600 ELSEAEVRQHREARPALLTSRLRFIPKPDGLRPIVNMDYVVGARTFRREKRAERLTSRVK 659

Db        580 ELSEAEVRRHREARPALLTSRLRFLPKPSGLRPIVNMDYIMGARTFHRDKKVQHLTSQLK 639

Qy        660 ALFSVLNYERARRPGLLGASVLGLDDIHRAWRTFVLRVRAQDPPPELYFVKVDVTGAYDT 719

Db        640 TLFSVLNYERARRPSLLGASMLGMDDIHRAWRTFVLRIRAQNPAPQLYFVKVDVTGAYDA 699

Qy        720 IPQDRLTEVIASIIKPQ-NTYCVRRYAVVQKAAHGHVRKAFKSH 762

Db        700 LPQDRLVEVIANVIRPQESTYCVRHYAVVQRTARGHVRKAFKRH 743
```

```
RESULT 70
AAW56109
ID   AAW56109 standard; protein; 564 AA.
XX
AC   AAW56109;
XX
DT   13-AUG-1998  (first entry)
XX
DE   Human telomerase reverse transcriptase 63 kDa clone 712562 protein.
XX
KW   Human; telomerase reverse transcriptase; hTRT; TRT; diagnosis; prognosis;
KW   cell proliferation; cancer; ageing; ribonucleoprotein.
XX
OS   Synthetic.
OS   Homo sapiens.
XX
FH   Key             Location/Qualifiers
FT   Misc-difference 102
FT                   /label= encoded by ARG
XX
PN   GB2317891-A.
XX
PD   08-APR-1998.
XX
PF   01-OCT-1997;   97GB-00020890.
XX
PR   01-OCT-1996;   96US-00724643.
PR   18-APR-1997;   97US-00844419.
PR   25-APR-1997;   97US-00846017.
PR   06-MAY-1997;   97US-00851843.
PR   09-MAY-1997;   97US-00854050.
PR   14-AUG-1997;   97US-00911312.
PR   14-AUG-1997;   97US-00912951.
PR   14-AUG-1997;   97US-00915503.
XX
PA   (GERO-) GERON CORP.
PA   (UYTE-) UNIV TECHNOLOGY CORP.
XX
PI   Cech TR,  Lingner J,  Nakamura T,  Chapman KB,  Morin GB,  Harley CB;
PI   Andrews WH;
XX
DR   WPI; 1998-171633/16.
DR   N-PSDB; AAV22426.
XX
PT   Pure and recombinant human Telomerase Reverse Transcriptase and its
PT   variants - are useful in the diagnosis, prognosis and treatment of cell
PT   proliferation conditions especially cancer and ageing.
XX
PS   Example 1; Fig 68; 387pp; English.
XX
CC   The present sequence is a human telomerase reverse transcriptase (hTRT)
CC   clone protein from the present invention. The present invention also
CC   describes the following methods: (A) determining whether a test compound
CC   is a modulator of hTRT, by detecting the change in hTRT recombinant
CC   protein or polynucleotide, on administration of the compound; (B)
CC   preparation of recombinant telomerase by contacting a protein preparation
CC   of hTRT with a telomerase RNA component; (C) detection of the hTRT RNA or
CC   protein in a sample by binding a relevant probe to the sample and
CC   detecting the complex formed or in the case of RNA detection, amplifying
CC   the product and correlating the presence of complex or amplification
CC   product with presence of hTRT in the sample; and (D) increasing the
CC   proliferation of a vertebrate cell by increasing hTRT expression; and (E)
CC   the use of an agent that causes an increase in cell vertebrate cell
CC   proliferation to create a medicament that inhibits ageing. A protein
CC   preparation of hTRT and the polynucleotide encoding hTRT can be used in
CC   the manufacture of medicaments for inhibiting the effect of ageing or
CC   cancer. Inhibitors of telomerase activity can be used to treat conditions
CC   that are associated with high telomerase activity. A protein preparation
CC   of hTRT can also be used in the new methods
XX
SQ   Sequence 564 AA;
```

```
  Query Match           35.0%;  Score 2088;  DB 2;  Length 564;
  Best Local Similarity   72.8%;  Pred. No. 1.7e-166;
  Matches  433;  Conservative   12;  Mismatches   38;  Indels  112;  Gaps    7;

Qy        549 MSVYVVELLRSFFYVTETTFQKNRLFFYRKSVWSKLQSIGIRQHLKRVQLRELSEAEVRQ 608

Db          1 MSVYVVELLRSFFYVTETTFQKNRLFFYRKSVWSKLQSIGIRQHLKRVQLRELSEAEVRQ 60

Qy        609 HREARPALLTSRLRFIPKPDGLRPIVNMDYVVGARTFRREKRAERLTSRVKALFSVLNYE 668

Db         61 HREARPALLTSRLRFIPKPDGLRPIVNMDYVVGARTFRREKXAERLTSRVKALFSVLNYE 120

Qy        669 RARRPGLLGASVLGLDDIHRAWRTFVLRVRAQDPPPELYFVKVDVTGAYDTIPQDRLTEV 728

Db        121 RARRPGLLGASVLGLDDIHRAWRTFVLRVRAQDPPPELYFVKVDVTGAYDTIPQDRLTEV 180

Qy        729 IASIIKPQNTYCVRRYAVVQKAAHGHVRKAFKSHVSTLTDLQPYMRQFVAHLQETSPLRD 788

Db        181 IASIIKPQNTYCVRRYAVVQKAAMG------------TSARP---------------- 210

Qy        789 AVVIEQSSSLNEASSGLFDVFLRFMCHHAVRIRGKSYVQCQGIPQGSILSTLLCSLCYGD 848

Db        211 ------------------------------SRATSYVQCQGIPQGSILSTLLCSLCYGD 239

Qy        849 MENKLFAGIRRDGLLLRLVDDFLLVTPHLTHAKTFLRTLVRGVPEYGCVVNLRKTVVNFP 908

Db        240 MENKLFAGIRRDGLLLRLVDDFLLVTPHLTHAKTFLRTLVRGVPEYGCVVNLRKTVVNFP 299

Qy        909 VEDEALGGTAFVQMPAHGLFPWCGLLLDTRTLEVQSDYSSYARTSIRASLTFNRGFKAGR 968

Db        300 VEDEALGGTAFVQMPAHGLFPWCGLLLDTRTLEVQSDYSSYARTSIRASLTFNRGFKAGR 359

Qy        969 NMRRKLFGVLRLKCHSLFLDLQVNSLQTVCTNIYKILLLQAYRFHACVLQLPFHQQVWKN 1028

Db        360 NMRRKLFGVLRLKCHSLFLDLQVNSLQTVCTNIYKILLLQAYRFHACVLQLPFHQQVWKN 419

Qy       1029 PTFFLRVISDTASLCYSIL---------------KAKNAGMSLGAKGAAGP--LPSEAVQ 1071

Db        420 PHF-----SCASSLTRLPLLLHPESQERRDVAGGQGRRRPSALRGRAVAVPPSIPAQADS 474

Qy       1072 WLCHQAFLLKLTRHRVTYVPLLGSLRTAQTQLSRKLPGTTLTALEAAANPALPSD 1126

Db        475 TPCH----------------------------LRATPGVTQDSPDAAESEA-PGD 500
```

```
RESULT 71
ADG90605
ID   ADG90605 standard; protein; 575 AA.
XX
AC   ADG90605;
XX
DT   25-MAR-2004  (first entry)
XX
DE   Rat TERT SEQ ID NO:8.
XX
KW   rat; immune response; telomerase reverse transcriptase; TERT; cytostatic;
KW   immunostimulant; cancer; cytotoxic T cell response.
XX
```

OS Rattus norvegicus.
XX
PN WO2004002408-A2.
XX
PD 08-JAN-2004.
XX
PF 24-JUN-2003; 2003WO-US019844.
XX
PR 27-JUN-2002; 2002US-0393295P.
XX
PA (GERO-) GERON CORP.
XX
PI Majumdar A, Ferber IA, Frolkis M, Wang Z;
XX
DR WPI; 2004-071946/07.
DR N-PSDB; ADG90604.
XX
PT Eliciting an immune response in a mammal specific for its own telomerase
PT reverse transcriptase (TERT), useful for treating or preventing cancer,
PT comprises administering a composition containing TERT of another
PT mammalian species.
XX
PS Claim 10; SEQ ID NO 8; 44pp; English.
XX
CC The invention relates to a novel method for eliciting an immune response
CC in a mammalian subject that is specific for its own telomerase reverse
CC transcriptase (TERT), comprising administering an immunogenic composition
CC containing a protein with at least 20 consecutive amino acids of TERT of
CC another mammalian species, or a nucleic acid encoding the protein. A
CC composition of the invention has cytostatic, and immunostimulant
CC activity. The protein or the nucleic acid encoding the protein is useful
CC in the manufacture of a medicament for the treatment of cancer in a human
CC or for eliciting a cytotoxic T cell response in a human.
XX
SQ Sequence 575 AA;

Query Match 33.8%; Score 2016; DB 8; Length 575;
Best Local Similarity 67.6%; Pred. No. 2e-160;
Matches 391; Conservative 71; Mismatches 110; Indels 6; Gaps 3;

```
Qy        558 RSFFYVTETTFQKNRLFFYRKSVWSKLQSIGIRQHLKRVQLRELSEAEVRQHREARPALL 617
              |||||:||:||||||||||||||||||||:||||:||:|||||: ||| |::   |:
Db          1 RSFFYITESTFQKNRLFFYRKSVWSKLQSIGVRQHLERVRLRELSQEEVRHHQDTWLAMP 60

Qy        618 TSRLRFIPKPDGLRPIVNMDYVVGARTFRREKRAERLTSRVKALFSVLNYERARRPGLLG 677
                |||||||:|||||||| | :| |   | |:|:  | |:| |||:|||| : | |:|
Db         61 ICRLRFIPKPNGLRPIVNMSYSMGTRALGRRKQAQHFTQRLKTLFSMLNYERTKHPHLMG 120

Qy        678 ASVLGLDDIHRAWRTFVLRVRAQDPPPELYFVKVDVTGAYDTIPQDRLTEVIASIIK-PQ 736
              :||||::||:| || ||||||| |  | :|||| ||||||| ||| :| ||:|::|:  :
Db        121 SSVLGMNDIYRTWRAFVLRVRALDQTPRMYFVKADVTGAYDAIPQGKLVEVVANMIRHSE 180

Qy        737 NTYCVRRYAVVQKAAHGHVRKAFKSHVSTLTDLQPYMRQFVAHLQET--SPLRDAVVIEQ 794
              :|||:|:||||:: : | | |:|:  |:||:|||||| ||: |||::  | ||::|||||
Db        181 STYCIRQYAVVRRDSQGQVHKSFRRQVTTLSDLQPYMGQFLKHLQDSDASALRNSVVIEQ 240

Qy        795 SSSLNEASSGLFDVFLRFMCHHAVRIRGKSYVQCQGIPQGSILSTLLCSLCYGDMENKLF 854
              | |:||:|| ||| || |: |  |:|  : | |||||||||| ||||||||:||||||||
Db        241 SISMNESSSSLFDFFLHFLRHSVVKIGDRCYTQCQGIPQGSSLSTLLCSLCFGDMENKLF 300

Qy        855 AGIRRDGLLLRLVDDFLLVTPHLTHAKTFLRTLVRGVPEYGCVVNLRKTVVNFPVEDEAL 914
              | ::||||||| ||||||||||  ||||| ||| |||||||::||:|||||||||   |
Db        301 AEVQRDGLLLRFVDDFLLVTPHLDQAKTFLSTLVHGVPEYGCMINLQKTVVNFPVEPGTL 360

Qy        915 GGTAFVQMPAHGLFPWCGLLLDTRTLEVQSDYSSYARTSIRASLTFNRGFKAGRNMRRKL 974
              || |  |:||| ||||||||||:||||  ||| ||:|||: ||||   ||||: || ||
Db        361 GGAAPYQLPAHCLFPWCGLLLDTQTLEVFCDYSGYAQTSIKTSLTFQSVFKAGKTMRNKL 420

Qy        975 FGVLRLKCHSLFLDLQVNSLQTVCTNIYKILLLQAYRFHACVLQLPFHQQVWKNPTFFLR 1034
              ||||||| ||||||||||||| ||||| ||||||||||:|||| |:| || ||||
Db        421 LSVLRLKCHGLFLDLQVNSLQTVCINIYKIFLLQAYRFHACVIQLPFDQRVRKNLTFFLG 480

Qy       1035 VISDTASLCYSILKAKNAGMSLGAKGAAGPLPSEAVQWLCHQAFLLKLTRHRVTYVPLLG 1094
```

```
              :||  || ||:||| || ||:| | |:   | ||  |||:|||||||  | | |  |||
Db        481 IISSQASCCYAILKVKNPGMTLKASGS---FPPEAAHWLCYQAFLLKLAAHSVIYKCLLG 537

Qy       1095 SLRTAQTQLSRKLPGTTLTALEAAANPALPSDFKTILD 1132
                |||||  | ||||  |:| |:|||:||| :||:||||
Db        538 PLRTAQKLLCRKLPEATMTILKAAADPALSTDFQTILD 575
```

RESULT 72
AAY00645
ID AAY00645 standard; protein; 348 AA.
XX
AC AAY00645;
XX
DT 26-JUL-1999 (first entry)
XX
DE Truncated telomerase (ver. 2) protein sequence.
XX
KW Telomerase; human; cancer; diagnosis; melanoma; skin cancer; leukaemia;
KW neuroblastoma; breast carcinoma; colon carcinoma; lymphoma; osteosarcoma;
KW smooth muscle cell hyperplasia; stem cell proliferation; Wilm's tumour;
KW stem cell differentiation; organ regeneration; organ differentiation.
XX
OS Homo sapiens.
OS Synthetic.
XX
PN WO9901560-A1.
XX
PD 14-JAN-1999.
XX
PF 01-JUL-1998; 98WO-US013835.
XX
PR 01-JUL-1997; 97US-0051410P.
PR 21-JUL-1997; 97US-0053018P.
PR 21-JUL-1997; 97US-0053329P.
PR 04-AUG-1997; 97US-0054642P.
PR 09-SEP-1997; 97US-0058287P.
XX
PA (CAMB-) CAMBIA BIOSYSTEMS LLC.
XX
PI Kilian A, Bowtell D;
XX
DR WPI; 1999-106060/09.
DR N-PSDB; AAX18273.
XX
PT New isolated vertebrate telomerase genes - used to develop products for
PT treating cancers or for organ regeneration, nerve cell or brain cell
PT growth following injury or bone marrow transplantation.
XX
PS Claim 4; Fig 11w; 134pp; English.
XX
CC This sequence is a truncated human telomerase of the invention. Primers
CC that amplify the telomerase coding sequence can be used in a method for
CC diagnosing cancer in a patient. The telomerase can be used for detection,
CC diagnosis and drug screening. Inhibitors of telomerase activity can be
CC used to treat cancers such as melanomas, other skin cancers,
CC neuroblastomas, breast carcinomas, colon carcinomas, leukaemias,
CC lymphomas, osteosarcomas or smooth muscle cell hyperplasias or skin
CC growths. Enhancers of telomerase may be used to stimulate stem cell
CC proliferation and differentiation (expansion of haematopoietic stem cells
CC could be administered in the bone marrow transplant context). As well,
CC many tissues have stem cells. Proliferation of these cells may be useful
CC in wound healing, hair growth, treatment of disease such as Wilm's
CC tumour, organ regeneration or differentiation after injury or diseases,
CC nerve cell or brain cell growth following injury. Note: The N-terminus of
CC this sequence can be replaced by the sequences shown in AAY00656-Y00658
XX
SQ Sequence 348 AA;

Query Match 31.3%; Score 1863; DB 2; Length 348;
Best Local Similarity 99.7%; Pred. No. 7.6e-148;
Matches 347; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

```
Qy          1 MPRAPRCRAVRSLLRSHYREVLPLATFVRRLGPQGWRLVQRGDPAAFRALVAQCLVCVPW 60
              |||||||||||||||| ||||||||||||||||||||||||||||||||||||||||||
Db          1 MPRAPRCRAVRSLLRSHTREVLPLATFVRRLGPQGWRLVQRGDPAAFRALVAQCLVCVPW 60

Qy         61 DARPPPAAPSFRQVSCLKELVARVLQRLCERGAKNVLAFGFALLDGARGGPPEAFTTSVR 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 DARPPPAAPSFRQVSCLKELVARVLQRLCERGAKNVLAFGFALLDGARGGPPEAFTTSVR 120

Qy        121 SYLPNTVTDALRGSGAWGLLLRRVGDDVLVHLLARCALFVLVAPSCAYQVCGPPLYQLGA 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 SYLPNTVTDALRGSGAWGLLLRRVGDDVLVHLLARCALFVLVAPSCAYQVCGPPLYQLGA 180

Qy        181 ATQARPPPHASGPRRRLGCERAWNHSVREAGVPLGLPAPGARRRGGSASRSLPLPKRPRR 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 ATQARPPPHASGPRRRLGCERAWNHSVREAGVPLGLPAPGARRRGGSASRSLPLPKRPRR 240

Qy        241 GAAPEPERTPVGQGSWAHPGRTRGPSDRGFCVVSPARPAEEATSLEGALSGTRHSHPSVG 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 GAAPEPERTPVGQGSWAHPGRTRGPSDRGFCVVSPARPAEEATSLEGALSGTRHSHPSVG 300

Qy        301 RQHHAGPPSTSRPPRPWDTPCPPVYAETKHFLYSSGDKEQLRPSFLLS 348
              ||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 RQHHAGPPSTSRPPRPWDTPCPPVYAETKHFLYSSGDKEQLRPSFLLS 348
```

RESULT 73
AAW47001
ID AAW47001 standard; protein; 538 AA.
XX
AC AAW47001;
XX
DT 13-AUG-1998 (first entry)
XX
DE Glutathione-S-transferase and hTRT fusion protein 1.
XX
KW Human; telomerase reverse transcriptase; hTRT; TRT; diagnosis; prognosis;
KW cell proliferation; cancer; ageing; ribonucleoprotein.
XX
OS Synthetic.
OS Homo sapiens.
XX

FH	Key	Location/Qualifiers
FT	Region	1. .220
FT		/note= "glutathione-S-transferase fragment"
FT	Misc-difference	221. .226
FT		/note= "thrombin cleavage sequence"
FT	Misc-difference	227. .231
FT		/note= "heart muscle protein kinase recognition sequence"
FT	Misc-difference	232. .236
FT		/note= "residues introduced by cloning"
FT	Region	237. .538
FT		/note= "hTRT protein fragment"

XX
PN GB2317891-A.
XX
PD 08-APR-1998.
XX
PF 01-OCT-1997; 97GB-00020890.
XX
PR 01-OCT-1996; 96US-00724643.
PR 18-APR-1997; 97US-00844419.
PR 25-APR-1997; 97US-00846017.
PR 06-MAY-1997; 97US-00851843.
PR 09-MAY-1997; 97US-00854050.
PR 14-AUG-1997; 97US-00911312.
PR 14-AUG-1997; 97US-00912951.
PR 14-AUG-1997; 97US-00915503.
XX
PA (GERO-) GERON CORP.
PA (UYTE-) UNIV TECHNOLOGY CORP.
XX
PI Cech TR, Lingner J, Nakamura T, Chapman KB, Morin GB, Harley CB;
PI Andrews WH;
XX
DR WPI; 1998-171633/16.
XX
PT Pure and recombinant human Telomerase Reverse Transcriptase and its
PT variants - are useful in the diagnosis, prognosis and treatment of cell
PT proliferation conditions especially cancer and ageing.
XX
PS Example 6; Page 224; 387pp; English.
XX
CC The present sequence represents a fusion protein from an example of the
CC present invention which describes human telomerase reverse transcriptase
CC (hTRT). The present invention also describes the following methods: (A)
CC determining whether a test compound is a modulator of hTRT, by detecting
CC the change in hTRT recombinant protein or polynucleotide, on
CC administration of the compound; (B) preparation of recombinant telomerase
CC by contacting a protein preparation of hTRT with a telomerase RNA
CC component; (C) detection of the hTRT RNA or protein in a sample by
CC binding a relevant probe to the sample and detecting the complex formed
CC or in the case of RNA detection, amplifying the product and correlating
CC the presence of complex or amplification product with presence of hTRT in
CC the sample; and (D) increasing the proliferation of a vertebrate cell by
CC increasing hTRT expression; and (E) the use of an agent that causes an
CC increase in cell vertebrate cell proliferation to create a medicament
CC that inhibits ageing. A protein preparation of hTRT and the
CC polynucleotide encoding hTRT can be used in the manufacture of
CC medicaments for inhibiting the effect of ageing or cancer. Inhibitors of
CC telomerase activity can be used to treat conditions that are associated
CC with high telomerase activity. A protein preparation of hTRT can also be
CC used in the new methods
XX
SQ Sequence 538 AA;

Query Match 25.8%; Score 1538; DB 2; Length 538;
Best Local Similarity 98.3%; Pred. No. 3.3e-120;
Matches 297; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

```
Qy        831 IPQGSILSTLLCSLCYGDMENKLFAGIRRDGLLLRLVDDFLLVTPHLTHAKTFLRTLVRG 890
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||| |||
Db        237 IPQGSILSTLLCSLCYGDMENKLFAGIRRDGLLLRLVDDFLLVTPHLTHAKTFLRTTVRG 296

Qy        891 VPEYGCVVNLRKTVVNFPVEDEALGGTAFVQMPAHGLFPWCGLLLDTRTLEVQSDYSSYA 950
              |||||||||||||||||||||||||||||||| ||||||||||||||||||||||||||
Db        297 VPEYGCVVNLRKTVVNFPVEDEALGGTAFVQMPARGLFPWCGLLLDTRTLEVQSDYSSYA 356

Qy        951 RTSIRASLTFNRGFKAGRNMRRKLFGVLRLKCHSLFLDLQVNSLQTVCTNIYKILLLQAY 1010
              |||||||:||||||:||||||||||||||||||||||||||||||||||||||||||||||
Db        357 RTSIRASVTFNRGFRAGRNMRRKLFGVLRLKCHSLFLDLQVNSLQTVCTNIYKILLLQAY 416

Qy       1011 RFHACVLQLPFHQQVWKNPTFFLRVISDTASLCYSILKAKNAGMSLGAKGAAGPLPSEAV 1070
              |||||||||| ||||||||||||||||||||||||||||||||||||||||||||||||||
Db        417 RFHACVLQLPFEQQVWKNPTFFLRVISDTASLCYSILKAKNAGMSLGAKGAAGPLPSEAV 476

Qy       1071 QWLCHQAFLLKLTRHRVTYVPLLGSLRTAQTQLSRKLPGTTLTALEAAANPALPSDFKTI 1130
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        477 QWLCHQAFLLKLTRHRVTYVPLLGSLRTAQTQLSRKLPGTTLTALEAAANPALPSDFKTI 536

Qy       1131 LD 1132
              ||
Db        537 LD 538
```

RESULT 74
AAW47004
ID AAW47004 standard; protein; 514 AA.
XX
AC AAW47004;
XX
DT 13-AUG-1998 (first entry)
XX
DE Glutathione-S-transferase and hTRT fusion protein 4.
XX
KW Human; telomerase reverse transcriptase; hTRT; TRT; diagnosis; prognosis;
KW cell proliferation; cancer; ageing; ribonucleoprotein.

```
XX
OS   Synthetic.
OS   Homo sapiens.
XX
FH   Key             Location/Qualifiers
FT   Region          1. .220
FT                   /note= "glutathione-S-transferase fragment"
FT   Region          237. .514
FT                   /note= "hTRT protein fragment"
XX
PN   GB2317891-A.
XX
PD   08-APR-1998.
XX
PF   01-OCT-1997;   97GB-00020890.
XX
PR   01-OCT-1996;   96US-00724643.
PR   18-APR-1997;   97US-00844419.
PR   25-APR-1997;   97US-00846017.
PR   06-MAY-1997;   97US-00851843.
PR   09-MAY-1997;   97US-00854050.
PR   14-AUG-1997;   97US-00911312.
PR   14-AUG-1997;   97US-00912951.
PR   14-AUG-1997;   97US-00915503.
XX
PA   (GERO-) GERON CORP.
PA   (UYTE-) UNIV TECHNOLOGY CORP.
XX
PI   Cech TR,  Lingner J,  Nakamura T,  Chapman KB,  Morin GB,  Harley CB;
PI   Andrews WH;
XX
DR   WPI; 1998-171633/16.
XX
PT   Pure and recombinant human Telomerase Reverse Transcriptase and its
PT   variants - are useful in the diagnosis, prognosis and treatment of cell
PT   proliferation conditions especially cancer and ageing.
XX
PS   Example 6; Page 226-227; 387pp; English.
XX
CC   The present sequence represents a fusion protein from an example of the
CC   present invention which describes human telomerase reverse transcriptase
CC   (hTRT). The present invention also describes the following methods: (A)
CC   determining whether a test compound is a modulator of hTRT, by detecting
CC   the change in hTRT recombinant protein or polynucleotide, on
CC   administration of the compound; (B) preparation of recombinant telomerase
CC   by contacting a protein preparation of hTRT with a telomerase RNA
CC   component; (C) detection of the hTRT RNA or protein in a sample by
CC   binding a relevant probe to the sample and detecting the complex formed
CC   or in the case of RNA detection, amplifying the product and correlating
CC   the presence of complex or amplification product with presence of hTRT in
CC   the sample; and (D) increasing the proliferation of a vertebrate cell by
CC   increasing hTRT expression; and (E) the use of an agent that causes an
CC   increase in cell vertebrate cell proliferation to create a medicament
CC   that inhibits ageing. A protein preparation of hTRT and the
CC   polynucleotide encoding hTRT can be used in the manufacture of
CC   medicaments for inhibiting the effect of ageing or cancer. Inhibitors of
CC   telomerase activity can be used to treat conditions that are associated
CC   with high telomerase activity. A protein preparation of hTRT can also be
CC   used in the new methods
XX
SQ   Sequence 514 AA;

  Query Match             25.3%;  Score 1506;  DB 2;  Length 514;
  Best Local Similarity   99.6%;  Pred. No. 1.5e-117;
  Matches  278;  Conservative    1;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        281 EATSLEGALSGTRHSHPSVGRQHHAGPPSTSRPPRPWDTPCPPVYAETKHFLYSSGDKEQ 340
              :||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        236 KATSLEGALSGTRHSHPSVGRQHHAGPPSTSRPPRPWDTPCPPVYAETKHFLYSSGDKEQ 295

Qy        341 LRPSFLLSSLRPSLTGARRLVETIFLGSRPWMPGTPRRLPRLPQRYWQMRPLFLELLGNH 400
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        296 LRPSFLLSSLRPSLTGARRLVETIFLGSRPWMPGTPRRLPRLPQRYWQMRPLFLELLGNH 355

Qy        401 AQCPYGVLLKTHCPLRAAVTPAAGVCAREKPQGSVAAPEEEDTDPRRLVQLLRQHSSPWQ 460
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        356 AQCPYGVLLKTHCPLRAAVTPAAGVCAREKPQGSVAAPEEEDTDPRRLVQLLRQHSSPWQ 415

Qy        461 VYGFVRACLRRLVPPGLWGSRHNERRFLRNTKKFISLGKHAKLSLQELTWKMSVRDCAWL 520
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        416 VYGFVRACLRRLVPPGLWGSRHNERRFLRNTKKFISLGKHAKLSLQELTWKMSVRDCAWL 475

Qy        521 RRSPGVGCVPAAEHRLREEILAKFLHWLMSVYVVELLRS 559
              |||||||||||||||||||||||||||||||||||||||
Db        476 RRSPGVGCVPAAEHRLREEILAKFLHWLMSVYVVELLRS 514


RESULT 75
AAO29774
ID   AAO29774 standard; protein; 291 AA.
XX
AC   AAO29774;
XX
DT   27-AUG-2003  (first entry)
XX
DE   hTRT MHC restricted epitope from clone 8.
XX
KW   Human; telomerase reverse transcriptase; MHC; tumour-associated antigen;
KW   hyperproliferative disease; major histocompatibility complex; hTRT; TAA;
KW   immune-mediated disease; systemic lupus erythematosus; protein therapy;
KW   Grave's disease; multiple sclerosis; atherosclerosis; cancer; diabetes;
KW   Crohn's disease; gene therapy; arthritis; epitope; vaccine; vasculitis;
KW   cell therapy.
XX
OS   Homo sapiens.
XX
FH   Key             Location/Qualifiers
FT   Region          34. .48
FT                   /note= "MHC-II restricted epitope fragment"
FT   Region          133. .147
FT                   /note= "MHC-II restricted epitope fragment"
FT   Region          227. .241
FT                   /note= "MHC-II restricted epitope fragment"
XX
PN   WO2003038047-A2.
XX
PD   08-MAY-2003.
XX
PF   29-OCT-2002; 2002WO-US034588.
XX
PR   29-OCT-2001; 2001US-0345012P.
XX
PA   (BAYU ) BAYLOR COLLEGE MEDICINE.
XX
PI   Chen S,  Zhaoyang Y,  Schroers R;
XX
DR   WPI; 2003-430511/40.
DR   N-PSDB; AAL60416.
XX
PT   New human telomerase reverse transcriptase tumor-associated MHC-I or MHC-
PT   II restricted polynucleotides and antigens, useful for treating cancers
PT   (e.g. lung or bone cancer or lymphomas), Crohn's disease or multiple
PT   sclerosis.
XX
PS   Claim 3; Fig 2C; 143pp; English.
XX
CC   The invention relates to human telomerase reverse transcriptase (hTRT)
CC   major histocompatibility complex (MHC)-I or MHC-II restricted tumour-
CC   associated antigens (TAA) and polynucleotides encoding such proteins. The
CC   invention is useful for treating hyperproliferative diseases such as
CC   cancer (e.g. lung cancer, head and neck cancer, pancreatic cancer, breast
CC   cancer, prostate cancer, renal cancer, bone cancer, testicular cancer,
CC   cervical cancer, gastrointestinal cancer, lymphomas, colon cancer, pre-
CC   neoplastic lesions in the lung, melanoma or bladder cancer) or immune-
CC   mediated diseases which include arthritis, Crohn's disease, vasculitis,
CC   Grave's disease, multiple sclerosis, atherosclerosis, diabetes, systemic
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```
CC   lupus erythematosus etc. The invention is used in gene therapy, protein
CC   therapy, cell therapy and also in the preparation of vaccines. The
CC   present sequence is hTRT MHC class I and II restricted epitope
XX
SQ   Sequence 291 AA;

  Query Match             25.0%;  Score 1490;  DB 6;  Length 291;
  Best Local Similarity   100.0%;  Pred. No. 1.5e-116;
  Matches  291;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        540 ILAKFLHWLMSVYVVELLRSFFYVTETTFQKNRLFFYRKSVWSKLQSIGIRQHLKRVQLR 599
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 ILAKFLHWLMSVYVVELLRSFFYVTETTFQKNRLFFYRKSVWSKLQSIGIRQHLKRVQLR 60

Qy        600 ELSEAEVRQHREARPALLTSRLRFIPKPDGLRPIVNMDYVVGARTFRREKRAERLTSRVK 659
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 ELSEAEVRQHREARPALLTSRLRFIPKPDGLRPIVNMDYVVGARTFRREKRAERLTSRVK 120

Qy        660 ALFSVLNYERARRPGLLGASVLGLDDIHRAWRTFVLRVRAQDPPPELYFVKVDVTGAYDT 719
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 ALFSVLNYERARRPGLLGASVLGLDDIHRAWRTFVLRVRAQDPPPELYFVKVDVTGAYDT 180

Qy        720 IPQDRLTEVIASIIKPQNTYCVRRYAVVQKAAHGHVRKAFKSHVSTLTDLQPYMRQFVAH 779
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 IPQDRLTEVIASIIKPQNTYCVRRYAVVQKAAHGHVRKAFKSHVSTLTDLQPYMRQFVAH 240

Qy        780 LQETSPLRDAVVIEQSSSLNEASSGLFDVFLRFMCHHAVRIRGKSYVQCQG 830
              |||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 LQETSPLRDAVVIEQSSSLNEASSGLFDVFLRFMCHHAVRIRGKSYVQCQG 291


RESULT 76
AAY43128
ID   AAY43128 standard; protein; 283 AA.
XX
AC   AAY43128;
XX
DT   20-DEC-1999  (first entry)
XX
DE   Human telomerase reverse transcriptase.
XX
KW   Human telomerase reverse transcriptase; hTERT; antibody; diagnosis;
KW   telomerase-related disease; cancer.
XX
OS   Homo sapiens.
XX
PN   WO9950407-A1.
XX
PD   07-OCT-1999.
XX
PF   26-MAR-1999;   99WO-JP001557.
XX
PR   26-MAR-1998;   98JP-00098486.
XX
PA   (KYOW ) KYOWA HAKKO KOGYO KK.
XX
PI   Hanai N,  Yamasaki M,  Shibata K,  Furuya A,  Mikuni O,  Anazawa H;
XX
DR   WPI; 1999-591316/50.
XX
PT   New monoclonal antibody recognizing human telomerase catalytic subunit
PT   (hTERT) useful for treating and diagnosing cancer.
XX
PS   Claim 2; Page 72-73; 78pp; Japanese.
XX
CC   This sequence represents the human telomerase reverse transcriptase
CC   (hTERT). The invention relates to a monoclonal antibody recognising the
CC   hTERT. The antibody can be used for the investigation, diagnosis and
CC   treatment of telomerase-related diseases, especially diseases in which
CC   telomerase expression is up-regulated e.g. cancers
XX
SQ   Sequence 283 AA;

  Query Match             24.2%;  Score 1444;  DB 2;  Length 283;
  Best Local Similarity   100.0%;  Pred. No. 1.1e-112;
  Matches  283;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        549 MSVYVVELLRSFFYVTETTFQKNRLFFYRKSVWSKLQSIGIRQHLKRVQLRELSEAEVRQ 608
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 MSVYVVELLRSFFYVTETTFQKNRLFFYRKSVWSKLQSIGIRQHLKRVQLRELSEAEVRQ 60

Qy        609 HREARPALLTSRLRFIPKPDGLRPIVNMDYVVGARTFRREKRAERLTSRVKALFSVLNYE 668
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 HREARPALLTSRLRFIPKPDGLRPIVNMDYVVGARTFRREKRAERLTSRVKALFSVLNYE 120

Qy        669 RARRPGLLGASVLGLDDIHRAWRTFVLRVRAQDPPPELYFVKVDVTGAYDTIPQDRLTEV 728
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 RARRPGLLGASVLGLDDIHRAWRTFVLRVRAQDPPPELYFVKVDVTGAYDTIPQDRLTEV 180

Qy        729 IASIIKPQNTYCVRRYAVVQKAAHGHVRKAFKSHVSTLTDLQPYMRQFVAHLQETSPLRD 788
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 IASIIKPQNTYCVRRYAVVQKAAHGHVRKAFKSHVSTLTDLQPYMRQFVAHLQETSPLRD 240

Qy        789 AVVIEQSSSLNEASSGLFDVFLRFMCHHAVRIRGKSYVQCQGI 831
              |||||||||||||||||||||||||||||||||||||||||||
Db        241 AVVIEQSSSLNEASSGLFDVFLRFMCHHAVRIRGKSYVQCQGI 283


RESULT 77
AAW47002
ID   AAW47002 standard; protein; 531 AA.
XX
AC   AAW47002;
XX
DT   13-AUG-1998  (first entry)
XX
DE   Glutathione-S-transferase and hTRT fusion protein 2.
XX
KW   Human; telomerase reverse transcriptase; hTRT; TRT; diagnosis; prognosis;
KW   cell proliferation; cancer; ageing; ribonucleoprotein.
XX
OS   Synthetic.
OS   Homo sapiens.
XX
FH   Key             Location/Qualifiers
FT   Region          1. .221
FT                   /note= "glutathione-S-transferase fragment"
FT   Region          249. .531
FT                   /note= "hTRT protein fragment"
XX
PN   GB2317891-A.
XX
PD   08-APR-1998.
XX
PF   01-OCT-1997;   97GB-00020890.
XX
PR   01-OCT-1996;   96US-00724643.
PR   18-APR-1997;   97US-00844419.
PR   25-APR-1997;   97US-00846017.
PR   06-MAY-1997;   97US-00851843.
PR   09-MAY-1997;   97US-00854050.
PR   14-AUG-1997;   97US-00911312.
PR   14-AUG-1997;   97US-00912951.
PR   14-AUG-1997;   97US-00915503.
XX
PA   (GERO-) GERON CORP.
PA   (UYTE-) UNIV TECHNOLOGY CORP.
XX
PI   Cech TR,  Lingner J,  Nakamura T,  Chapman KB,  Morin GB,  Harley CB;
PI   Andrews WH;
XX
DR   WPI; 1998-171633/16.
XX
PT   Pure and recombinant human Telomerase Reverse Transcriptase and its
PT   variants - are useful in the diagnosis, prognosis and treatment of cell
PT   proliferation conditions especially cancer and ageing.
```

```
XX
PS   Example 6; Page 225; 387pp; English.
XX
CC   The present sequence represents a fusion protein from an example of the
CC   present invention which describes human telomerase reverse transcriptase
CC   (hTRT). The present invention also describes the following methods: (A)
CC   determining whether a test compound is a modulator of hTRT, by detecting
CC   the change in hTRT recombinant protein or polynucleotide, on
CC   administration of the compound; (B) preparation of recombinant telomerase
CC   by contacting a protein preparation of hTRT with a telomerase RNA
CC   component; (C) detection of the hTRT RNA or protein in a sample by
CC   binding a relevant probe to the sample and detecting the complex formed
CC   or in the case of RNA detection, amplifying the product and correlating
CC   the presence of complex or amplification product with presence of hTRT in
CC   the sample; and (D) increasing the proliferation of a vertebrate cell by
CC   increasing hTRT expression; and (E) the use of an agent that causes an
CC   increase in cell vertebrate cell proliferation to create a medicament
CC   that inhibits ageing. A protein preparation of hTRT and the
CC   polynucleotide encoding hTRT can be used in the manufacture of
CC   medicaments for inhibiting the effect of ageing or cancer. Inhibitors of
CC   telomerase activity can be used to treat conditions that are associated
CC   with high telomerase activity. A protein preparation of hTRT can also be
CC   used in the new methods
XX
SQ   Sequence 531 AA;

  Query Match             24.1%;  Score 1439;  DB 2;  Length 531;
  Best Local Similarity   92.6%;  Pred. No. 6.9e-112;
  Matches  287;  Conservative    1;  Mismatches   16;  Indels    6;  Gaps    1;

Qy        522 RSPGVGCVPAAEHRLREEILAKFLHWLMSVYVVELLRSFFYVTETTFQKNRLFFYRKSVW 581
              |   || |    |     :        ||||||||||||||||||||||||||| |||
Db        228 RRASVGSVHHHHHHHHHGSVTK------MSVYVVELLRSFFYVTETTFQKNRLFFYRPSVW 281

Qy        582 SKLQSIGIRQHLKRVQLRELSEAEVRQHREARPALLTSRLRFIPKPDGLRPIVNMDYVVG 641
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        282 SKLQSIGIRQHLKRVQLRELSEAEVRQHREARPALLTSRLRFIPKPDGLRPIVNMDYVVG 341

Qy        642 ARTFRREKRAERLTSRVKALFSVLNYERARRPGLLGASVLGLDDIHRAWRTFVLRVRAQD 701
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        342 ARTFRREKRAERLTSRVKALFSVLNYERARRPGLLGASVLGLDDIHRAWRTFVLRVRAQD 401

Qy        702 PPPELYFVKVDVTGAYDTIPQDRLTEVIASIIKPQNTYCVRRYAVVQKAAHGHVRKAFKS 761
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        402 PPPELYFVKVDVTGAYDTIPQDRLTEVIASIIKPQNTYCVRRYAVVQKAAHGHVRKAFKS 461

Qy        762 HVSTLTDLQPYMRQFVAHLQETSPLRDAVVIEQSSSLNEASSGLFDVFLRFMCHHAVRIR 821
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        462 HVSTLTDLQPYMRQFVAHLQETSPLRDAVVIEQSSSLNEASSGLFDVFLRFMCHHAVRIR 521

Qy        822 GKSYVQCQGI 831
              ||||||||||
Db        522 GKSYVQCQGI 531


RESULT 78
AAW47005
ID   AAW47005 standard; protein; 516 AA.
XX
AC   AAW47005;
XX
DT   13-AUG-1998  (first entry)
XX
DE   Glutathione-S-transferase and hTRT fusion protein 5.
XX
KW   Human; telomerase reverse transcriptase; hTRT; TRT; diagnosis; prognosis;
KW   cell proliferation; cancer; ageing; ribonucleoprotein.
XX
OS   Synthetic.
OS   Homo sapiens.
XX
FH   Key             Location/Qualifiers
FT   Region          1. .220
FT                   /note= "glutathione-S-transferase fragment"
FT   Region          237. .516
FT                   /note= "hTRT protein fragment"
XX
PN   GB2317891-A.
XX
PD   08-APR-1998.
XX
PF   01-OCT-1997;   97GB-00020890.
XX
PR   01-OCT-1996;   96US-00724643.
PR   18-APR-1997;   97US-00844419.
PR   25-APR-1997;   97US-00846017.
PR   06-MAY-1997;   97US-00851843.
PR   09-MAY-1997;   97US-00854050.
PR   14-AUG-1997;   97US-00911312.
PR   14-AUG-1997;   97US-00912951.
PR   14-AUG-1997;   97US-00915503.
XX
PA   (GERO-) GERON CORP.
PA   (UYTE-) UNIV TECHNOLOGY CORP.
XX
PI   Cech TR,  Lingner J,  Nakamura T,  Chapman KB,  Morin GB,  Harley CB;
PI   Andrews WH;
XX
DR   WPI; 1998-171633/16.
XX
PT   Pure and recombinant human Telomerase Reverse Transcriptase and its
PT   variants - are useful in the diagnosis, prognosis and treatment of cell
PT   proliferation conditions especially cancer and ageing.
XX
PS   Example 6; Page 227; 387pp; English.
XX
CC   The present sequence represents a fusion protein from an example of the
CC   present invention which describes human telomerase reverse transcriptase
CC   (hTRT). The present invention also describes the following methods: (A)
CC   determining whether a test compound is a modulator of hTRT, by detecting
CC   the change in hTRT recombinant protein or polynucleotide, on
CC   administration of the compound; (B) preparation of recombinant telomerase
CC   by contacting a protein preparation of hTRT with a telomerase RNA
CC   component; (C) detection of the hTRT RNA or protein in a sample by
CC   binding a relevant probe to the sample and detecting the complex formed
CC   or in the case of RNA detection, amplifying the product and correlating
CC   the presence of complex or amplification product with presence of hTRT in
CC   the sample; and (D) increasing the proliferation of a vertebrate cell by
CC   increasing hTRT expression; and (E) the use of an agent that causes an
CC   increase in cell vertebrate cell proliferation to create a medicament
CC   that inhibits ageing. A protein preparation of hTRT and the
CC   polynucleotide encoding hTRT can be used in the manufacture of
CC   medicaments for inhibiting the effect of ageing or cancer. Inhibitors of
CC   telomerase activity can be used to treat conditions that are associated
CC   with high telomerase activity. A protein preparation of hTRT can also be
CC   used in the new methods
XX
SQ   Sequence 516 AA;

  Query Match             23.8%;  Score 1417.5;  DB 2;  Length 516;
  Best Local Similarity   96.8%;  Pred. No. 4.3e-110;
  Matches  276;  Conservative    2;  Mismatches    2;  Indels    5;  Gaps    5;

Qy          1 MPRAPRCRAVRSLLRSHYREVLPLATFVRRLGPQGWRLVQRGDPAAFRALVAQCLVCVPW 60
              |||||||||||||| |||||||||||||||||||||||||||||||||||||||||||||
Db        237 MPRAPRCRAVRSLL-SHYREVLPLATFVRRLGPQGWRLVQRGDPAAFRALVAQCLVCVPW 295

Qy         61 DARPPPAAPSFRQVSCLKELVARVLQRLCERGAKNVLAFGFALLDGARGGPPEAFTTSVR 120
              ||| |||||||||||||||||||||||||:||||||||||||||||||| |||||
Db        296 DAR-PPAAPSFRQVSCLKELVARVLQRLCERGARNVLAFGFALLDGARGGPPEA-TTSVR 353

Qy        121 SYLPNTVTDALRGSGAWGLLLRRVGDDVLVHLLARCALFVLVAPSCAYQVCGPPLYQLGA 180
              |||||||||||||||||||||||||||||||||||||||||||| ||||||||||||||
Db        354 SYLPNTVTDALRGSGAWGLLLRRVGDDVLVHLLARCALFVLVAP-CAYQVCGPPLYQLGA 412

Qy        181 ATQARPPPHASGPRRRLGCERAWNHSVREAGVPLGLPAPGARRRGGSASRSLPLPKRPRR 240
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                |||||||| |||||||||||||||||||||||||||||||||||||||||||||||:||||
Db        413 ATQARPPPEASGPRRRLGCERAWNHSVREAGVPLGLPAPGARRRGGSASRSLPLPERPRR 472

Qy        241 GAAPEPERTPVGQGSWAHPGRTRGPSDRGFCVVSPARPAEEATSL 285
              |||||||||||||||||||||||||||||| ||||||||||||
Db        473 GAAPEPERTPVGQGSWAHPGRTRGPSDRGFC-WSPARPAEEATSL 516


RESULT 79
AAW47003
ID   AAW47003 standard; protein; 514 AA.
XX
AC   AAW47003;
XX
DT   13-AUG-1998  (first entry)
XX
DE   Glutathione-S-transferase and hTRT fusion protein 3.
XX
KW   Human; telomerase reverse transcriptase; hTRT; TRT; diagnosis; prognosis;
KW   cell proliferation; cancer; ageing; ribonucleoprotein.
XX
OS   Synthetic.
OS   Homo sapiens.
XX
FH   Key             Location/Qualifiers
FT   Region          1. .220
FT                   /note= "glutathione-S-transferase fragment"
FT   Region          238. .514
FT                   /note= "hTRT protein fragment"
XX
PN   GB2317891-A.
XX
PD   08-APR-1998.
XX
PF   01-OCT-1997;   97GB-00020890.
XX
PR   01-OCT-1996;   96US-00724643.
PR   18-APR-1997;   97US-00844419.
PR   25-APR-1997;   97US-00846017.
PR   06-MAY-1997;   97US-00851843.
PR   09-MAY-1997;   97US-00854050.
PR   14-AUG-1997;   97US-00911312.
PR   14-AUG-1997;   97US-00912951.
PR   14-AUG-1997;   97US-00915503.
XX
PA   (GERO-) GERON CORP.
PA   (UYTE-) UNIV TECHNOLOGY CORP.
XX
PI   Cech TR,  Lingner J,  Nakamura T,  Chapman KB,  Morin GB,  Harley CB;
PI   Andrews WH;
XX
DR   WPI; 1998-171633/16.
XX
PT   Pure and recombinant human Telomerase Reverse Transcriptase and its
PT   variants - are useful in the diagnosis, prognosis and treatment of cell
PT   proliferation conditions especially cancer and ageing.
XX
PS   Example 6; Page 226; 387pp; English.
XX
CC   The present sequence represents a fusion protein from an example of the
CC   present invention which describes human telomerase reverse transcriptase
CC   (hTRT). The present invention also describes the following methods: (A)
CC   determining whether a test compound is a modulator of hTRT, by detecting
CC   the change in hTRT recombinant protein or polynucleotide, on
CC   administration of the compound; (B) preparation of recombinant telomerase
CC   by contacting a protein preparation of hTRT with a telomerase RNA
CC   component; (C) detection of the hTRT RNA or protein in a sample by
CC   binding a relevant probe to the sample and detecting the complex formed
CC   or in the case of RNA detection, amplifying the product and correlating
CC   the presence of complex or amplification product with presence of hTRT in
CC   the sample; and (D) increasing the proliferation of a vertebrate cell by
CC   increasing hTRT expression; and (E) the use of an agent that causes an
CC   increase in cell vertebrate cell proliferation to create a medicament
CC   that inhibits ageing. A protein preparation of hTRT and the
CC   polynucleotide encoding hTRT can be used in the manufacture of
CC   medicaments for inhibiting the effect of ageing or cancer. Inhibitors of
CC   telomerase activity can be used to treat conditions that are associated
CC   with high telomerase activity. A protein preparation of hTRT can also be
CC   used in the new methods
XX
SQ   Sequence 514 AA;

  Query Match             22.3%;  Score 1330.5;  DB 2;  Length 514;
  Best Local Similarity   81.2%;  Pred. No. 9e-103;
  Matches  286;  Conservative    8;  Mismatches   35;  Indels   23;  Gaps   11;

Qy        487 FLRNTKKFISLGKHAKLSLQELTWKMSVRDCAWLR------RSPGVGCVPAAEHRLREEI 540
              |:  :    :|: | | : : | :      |           |    ||    |
Db        179 FKKRIEAIPQIDKYLK-SSKYIAWPLQ----GWQATFGGGDHPPKSDLVPPGSRRASVGS 233

Qy        541 LAKFLHWLMSVYVVELLRSFFYVTETTFQKNRLFFYRKSVWSKLQSIGIRQHLKRVQLRE 600
              : |     |||||||||||||||||||||||||||| ||||||||||||||||||||||
Db        234 VTK-----MSVYVVELLRSFFYVTETTFQKNRLFFYRPSVWSKLQSIGIRQHLKRVQLRE 288

Qy        601 LSEAEVRQH-REARPALLTSRLRFIPKPDGLRPIVNMDYVVGARTFRREKRAERLTSRVK 659
              |||| |||| |||||||||||||||||||||||||||||||||||||||||||||||||| |
Db        289 LSEA-VRQHEREARPALLTSRLRFIPKPDGLRPIVNMDYVVGARTFRREKRAERLTSR-K 346

Qy        660 ALFSVLNYERARRPGLLGASVLGLDDIHRAWRTFVLRVRAQDPPPELYFVKVDVTGAYDT 719
              |||||||||||||||||||||||||||||||||||||||||||||| ||||||||||||
Db        347 ALFSVLNYERARRPGLLGASVLGLDDIHRAWRTFVLRVRAQDPPPE-YFVKVDVTGAYDT 405

Qy        720 IPQDRLTEVIASIIKPQNTYCVRRYAVVQKAAHGHVRKAFKSHVSTLTDLQPYMRQFVAH 779
              |||||||||||||||||||||||||||  |||||| ||||||||||||||||||||||||
Db        406 IPQDRLTEVIASIIKPQNTYCVRRYA-WQKAAHG-VRKAFKSHVSTLTDLQPYMRQFVAH 463

Qy        780 LQETSPLRDAVVIEQSSSLNEASSGLFDVFLRFMCHHAVRIRGKSYVQCQGI 831
              |||||||||||||||||||| ||||||||||||||||||||||||||||||
Db        464 LQETSPLRDAVVIEQSSSLNEA-SGLFDVFLRFMCHHAVRIRGKSYVQCQGI 514


RESULT 80
ADG85224
ID   ADG85224 standard; protein; 250 AA.
XX
AC   ADG85224;
XX
DT   11-MAR-2004  (first entry)
XX
DE   Human telomerase reverse transcriptase.
XX
KW   telomerase catalytic activity;
KW   hydrogen peroxide-induced cellular senescence; proliferative disease;
KW   cancer; human; telomerase reverse transcriptase; enzyme.
XX
OS   Homo sapiens.
XX
PN   US2003225027-A1.
XX
PD   04-DEC-2003.
XX
PF   30-MAY-2003; 2003US-00449565.
XX
PR   31-MAY-2002; 2002US-0384806P.
XX
PA   (HUAN/) HUANG J.
PA   (HUAN/) HUANG C.
PA   (LINM/) LIN M C M.
PA   (KUNG/) KUNG H.
XX
PI   Huang JJ,  Huang C,  Lin MCM,  Kung H;
XX
DR   WPI; 2004-089418/09.
DR   N-PSDB; ADG85223.
XX
PT   New human telomerase reverse transcriptase polypeptide, useful in
```

```
PT   preparing a composition for treating or preventing proliferative disease,
PT   e.g., cancer.
XX
PS   Claim 3; SEQ ID NO 2; 38pp; English.
XX
CC   The invention relates to a new polypeptide which lacks telomerase
CC   catalytic activity or inhibitory effect on telomerase catalytic activity
CC   in a cell and has the ability to sensitize HeLa cells to hydrogen
CC   peroxide-induced cellular senescence. The polypeptide is useful in
CC   preparing a composition for treating or preventing proliferative disease
CC   e.g. cancer. The present sequence represents the amino acid sequence of
CC   human telomerase reverse transcriptase.
XX
SQ   Sequence 250 AA;

  Query Match             21.7%;  Score 1296;  DB 8;  Length 250;
  Best Local Similarity   100.0%;  Pred. No. 2.6e-100;
  Matches  250;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        883 FLRTLVRGVPEYGCVVNLRKTVVNFPVEDEALGGTAFVQMPAHGLFPWCGLLLDTRTLEV 942
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 FLRTLVRGVPEYGCVVNLRKTVVNFPVEDEALGGTAFVQMPAHGLFPWCGLLLDTRTLEV 60

Qy        943 QSDYSSYARTSIRASLTFNRGFKAGRNMRRKLFGVLRLKCHSLFLDLQVNSLQTVCTNIY 1002
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 QSDYSSYARTSIRASLTFNRGFKAGRNMRRKLFGVLRLKCHSLFLDLQVNSLQTVCTNIY 120

Qy       1003 KILLLQAYRFHACVLQLPFHQQVWKNPTFFLRVISDTASLCYSILKAKNAGMSLGAKGAA 1062
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 KILLLQAYRFHACVLQLPFHQQVWKNPTFFLRVISDTASLCYSILKAKNAGMSLGAKGAA 180

Qy       1063 GPLPSEAVQWLCHQAFLLKLTRHRVTYVPLLGSLRTAQTQLSRKLPGTTLTALEAAANPA 1122
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 GPLPSEAVQWLCHQAFLLKLTRHRVTYVPLLGSLRTAQTQLSRKLPGTTLTALEAAANPA 240

Qy       1123 LPSDFKTILD 1132
              ||||||||||
Db        241 LPSDFKTILD 250


RESULT 81
AAW46998
ID   AAW46998 standard; protein; 259 AA.
XX
AC   AAW46998;
XX
DT   13-AUG-1998  (first entry)
XX
DE   Human telomerase reverse transcriptase protein from cDNA clone 712562.
XX
KW   Human; telomerase reverse transcriptase; hTRT; TRT; diagnosis; prognosis;
KW   cell proliferation; cancer; ageing; ribonucleoprotein.
XX
OS   Homo sapiens.
XX
PN   GB2317891-A.
XX
PD   08-APR-1998.
XX
PF   01-OCT-1997;   97GB-00020890.
XX
PR   01-OCT-1996;   96US-00724643.
PR   18-APR-1997;   97US-00844419.
PR   25-APR-1997;   97US-00846017.
PR   06-MAY-1997;   97US-00851843.
PR   09-MAY-1997;   97US-00854050.
PR   14-AUG-1997;   97US-00911312.
PR   14-AUG-1997;   97US-00912951.
PR   14-AUG-1997;   97US-00915503.
XX
PA   (GERO-) GERON CORP.
PA   (UYTE-) UNIV TECHNOLOGY CORP.
XX
PI   Cech TR,  Lingner J,  Nakamura T,  Chapman KB,  Morin GB,  Harley CB;
PI   Andrews WH;
XX
DR   WPI; 1998-171633/16.
DR   N-PSDB; AAV22379.
XX
PT   Pure and recombinant human Telomerase Reverse Transcriptase and its
PT   variants - are useful in the diagnosis, prognosis and treatment of cell
PT   proliferation conditions especially cancer and ageing.
XX
PS   Example 1; Fig 19; 387pp; English.
XX
CC   The present sequence represents a human telomerase reverse transcriptase
CC   (hTRT) protein from a cDNA clone from the present invention. The present
CC   invention also describes the following methods: (A) determining whether a
CC   test compound is a modulator of hTRT, by detecting the change in hTRT
CC   recombinant protein or polynucleotide, on administration of the compound;
CC   (B) preparation of recombinant telomerase by contacting a protein
CC   preparation of hTRT with a telomerase RNA component; (C) detection of the
CC   hTRT RNA or protein in a sample by binding a relevant probe to the sample
CC   and detecting the complex formed or in the case of RNA detection,
CC   amplifying the product and correlating the presence of complex or
CC   amplification product with presence of hTRT in the sample; and (D)
CC   increasing the proliferation of a vertebrate cell by increasing hTRT
CC   expression; and (E) the use of an agent that causes an increase in cell
CC   vertebrate cell proliferation to create a medicament that inhibits
CC   ageing. A protein preparation of hTRT and the polynucleotide encoding
CC   hTRT can be used in the manufacture of medicaments for inhibiting the
CC   effect of ageing or cancer. Inhibitors of telomerase activity can be used
CC   to treat conditions that are associated with high telomerase activity. A
CC   protein preparation of hTRT can also be used in the new methods
XX
SQ   Sequence 259 AA;

  Query Match             18.4%;  Score 1096;  DB 2;  Length 259;
  Best Local Similarity   100.0%;  Pred. No. 1.9e-83;
  Matches  215;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        549 MSVYVVELLRSFFYVTETTFQKNRLFFYRKSVWSKLQSIGIRQHLKRVQLRELSEAEVRQ 608
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 MSVYVVELLRSFFYVTETTFQKNRLFFYRKSVWSKLQSIGIRQHLKRVQLRELSEAEVRQ 60

Qy        609 HREARPALLTSRLRFIPKPDGLRPIVNMDYVVGARTFRREKRAERLTSRVKALFSVLNYE 668
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 HREARPALLTSRLRFIPKPDGLRPIVNMDYVVGARTFRREKRAERLTSRVKALFSVLNYE 120

Qy        669 RARRPGLLGASVLGLDDIHRAWRTFVLRVRAQDPPPELYFVKVDVTGAYDTIPQDRLTEV 728
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 RARRPGLLGASVLGLDDIHRAWRTFVLRVRAQDPPPELYFVKVDVTGAYDTIPQDRLTEV 180

Qy        729 IASIIKPQNTYCVRRYAVVQKAAHGHVRKAFKSHV 763
              |||||||||||||||||||||||||||||||||||
Db        181 IASIIKPQNTYCVRRYAVVQKAAHGHVRKAFKSHV 215


RESULT 82
AAO29775
ID   AAO29775 standard; protein; 174 AA.
XX
AC   AAO29775;
XX
DT   27-AUG-2003  (first entry)
XX
DE   hTRT MHC restricted epitope from clone 35.
XX
KW   Human; telomerase reverse transcriptase; MHC; tumour-associated antigen;
KW   hyperproliferative disease; major histocompatibility complex; hTRT; TAA;
KW   immune-mediated disease; systemic lupus erythematosus; protein therapy;
KW   Grave's disease; multiple sclerosis; atherosclerosis; cancer; diabetes;
KW   Crohn's disease; gene therapy; arthritis; epitope; vaccine; vasculitis;
KW   cell therapy.
XX
OS   Homo sapiens.
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XX
FH   Key             Location/Qualifiers
FT   Region          50. .64
FT                   /note= "MHC-II restricted epitope fragment"
FT   Region          86. .100
FT                   /note= "MHC-II restricted epitope fragment"
FT   Misc-difference 173. .174
FT                   /note= "Encoded by AAG"
XX
PN   WO2003038047-A2.
XX
PD   08-MAY-2003.
XX
PF   29-OCT-2002; 2002WO-US034588.
XX
PR   29-OCT-2001; 2001US-0345012P.
XX
PA   (BAYU ) BAYLOR COLLEGE MEDICINE.
XX
PI   Chen S,  Zhaoyang Y,  Schroers R;
XX
DR   WPI; 2003-430511/40.
DR   N-PSDB; AAL60417.
XX
PT   New human telomerase reverse transcriptase tumor-associated MHC-I or MHC-
PT   II restricted polynucleotides and antigens, useful for treating cancers
PT   (e.g. lung or bone cancer or lymphomas), Crohn's disease or multiple
PT   sclerosis.
XX
PS   Claim 5; Fig 2C; 143pp; English.
XX
CC   The invention relates to human telomerase reverse transcriptase (hTRT)
CC   major histocompatibility complex (MHC)-I and MHC-II restricted tumour-
CC   associated antigens (TAA) and polynucleotides encoding such proteins. The
CC   invention is useful for treating hyperproliferative diseases such as
CC   cancer (e.g. lung cancer, head and neck cancer, pancreatic cancer, breast
CC   cancer, prostate cancer, renal cancer, bone cancer, testicular cancer,
CC   cervical cancer, gastrointestinal cancer, lymphomas, colon cancer, pre-
CC   neoplastic lesions in the lung, melanoma or bladder cancer) or immune-
CC   mediated diseases which include arthritis, Crohn's disease, vasculitis,
CC   Grave's disease, multiple sclerosis, atherosclerosis, diabetes, systemic
CC   lupus erythematosus etc. The invention is used in gene therapy, protein
CC   therapy, cell therapy and also in the preparation of vaccines. The
CC   present sequence is hTRT MHC class I and II restricted epitope
XX
SQ   Sequence 174 AA;

  Query Match             15.2%;  Score 905;  DB 6;  Length 174;
  Best Local Similarity   100.0%;  Pred. No. 1.3e-67;
  Matches  174;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        831 IPQGSILSTLLCSLCYGDMENKLFAGIRRDGLLLRLVDDFLLVTPHLTHAKTFLRTLVRG 890
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 IPQGSILSTLLCSLCYGDMENKLFAGIRRDGLLLRLVDDFLLVTPHLTHAKTFLRTLVRG 60

Qy        891 VPEYGCVVNLRKTVVNFPVEDEALGGTAFVQMPAHGLFPWCGLLLDTRTLEVQSDYSSYA 950
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 VPEYGCVVNLRKTVVNFPVEDEALGGTAFVQMPAHGLFPWCGLLLDTRTLEVQSDYSSYA 120

Qy        951 RTSIRASLTFNRGFKAGRNMRRKLFGVLRLKCHSLFLDLQVNSLQTVCTNIYKI 1004
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 RTSIRASLTFNRGFKAGRNMRRKLFGVLRLKCHSLFLDLQVNSLQTVCTNIYKI 174


RESULT 83
AAE00431
ID   AAE00431 standard; protein; 379 AA.
XX
AC   AAE00431;
XX
DT   19-JUN-2001  (first entry)
XX
DE   Consensus sequence of telomerase reverse transcriptase (TERT) protein.
XX
KW   Telomerase reverse transcriptase; TERT; ever shorter telomere; EST;
KW   therapy; stomach cancer; malaria; vaginal candidiasis.
XX
OS   Unidentified.
XX
FH   Key             Location/Qualifiers
FT   Misc-difference 1
FT                   /label= Unknown
FT   Misc-difference 5
FT                   /label= Unknown
FT   Misc-difference 6
FT                   /label= Unknown
FT   Misc-difference 7
FT                   /label= Unknown
FT   Misc-difference 11
FT                   /label= Unknown
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FT   Misc-difference 44
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FT   Misc-difference 61
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FT   Misc-difference 108
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FT   Misc-difference 130
FT                   /label= Unknown
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FT                   /label= Unknown
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FT                   /label= Unknown
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FT   Misc-difference 188
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FT   Misc-difference 367
FT                   /label= Unknown
XX
PN   WO200127287-A2.
XX
PD   19-APR-2001.
XX
PF   10-OCT-2000; 2000WO-US027825.
```

Query Match 12.0%; Score 713; DB 4; Length 379;
Best Local Similarity 39.3%; Pred. No. 5.8e-51;
Matches 194; Conservative 31; Mismatches 137; Indels 132; Gaps 13;

```
Qy      451 LLRQHSSPWQVYGFVRACLRRLVPPGLWGSRHNERRFLRNTKKFISLGKHAKLSLQELTW 510
Db       15 LLSYXSXXXQVXNFLRXILXKLVPXXLWGXRHNKKIFLKNLKKFL-LXKYEXLSLQELMX 73

Qy      511 KMSVRDCAWLRRSPGVGCVPAAEHRLREEILAKFLHWLMSVYVVELLRSFFYVTETTFQK 570
Db       74 KIKVR----------------------XILAKFLFWLFDXLVVXLLRSFFYITETTXXX 110

Qy      571 NRLFFYRKSVWSKLQSIGIRQHLKRVQLRELSEAEVRQHREARPALLTSRLRFIPKP-DG 629
Db      111 XXLFYYRK-IWXXLXRIXFIXXLXK-XLRELQEKEVR----------XGKLRLIPKKXTX 158

Qy      630 LRPIVNMDYVVGARTFRREKRAERLTSRVKALFSVLNYERARRPGLLGASVLGLDDIHRA 689
Db      159 FRPIVNMXRKVVXRXLKXMTXNQXL---VXTLXMLKNLKXXXXXXXLGXSVXXXDDIMRR 215

Qy      690 WRTFVLRVRAQDPPPELYFVKVDVTGAYDTIPQDRLTEVIASIIKPQNTYCVRRYAVVQK 749
Db      216 WXXFVXKWRX----PKLYFVKVDIKXCYDTIXQDRLVRVLKXXIK--------------- 256

Qy      750 AAHGHVRKAFKSHVSTLTDLQPYMRQFVAHLQETSPLRDAVVIEQSSSLNEASSGLFDVF 809
```

```
                                          | |  ||:|||||
Db        257 ----------------------------XXEXSLXRDSVVIEQX---------- 272

Qy        810 LRFMCHHAVRIRGKSYVQCQGIPQGSILSTLLCSLCYGDMENKLFAG-IRRDGLLLRLVD 868
                          | | :||||||| |||:|||| |||:| : :   :||| |||||||
Db        273 ----------XYKQXKGIPQGSSLSTILCSLYYGDLEXEEYXQFLRRDXLLLRLVD 318

Qy        869 DFLLVTPHLTHAKTFLRTLVR-GVPEYGCVVNLRKTVVNFPVEDEALGGTAFVQMPAHGL 927
              ||||:|    :|| ||  ||| |   ||  ||| ||||||           ||  | |
Db        319 DFLLITXXXNNAKXFLXLLVRXGXXXYGFKVNLXKTVVNF----------QMXXHXL 365

Qy        928 FPWCGLLLDTRTLE 941
                | || :| ||||
Db        366 MXWIGLSIDIRTLE 379
```

RESULT 84
ABB99681
ID ABB99681 standard; protein; 174 AA.
XX
AC ABB99681;
XX
DT 28-MAR-2003 (first entry)
XX
DE Splice variant of a human telomerase reverse transcriptase fragment.
XX
KW Human; telomerase reverse transcriptase; hTERT; T cell response; vaccine;
KW cancer.
XX
OS Homo sapiens.
XX
PN WO200294312-A1.
XX
PD 28-NOV-2002.
XX
PF 16-MAY-2002; 2002WO-NO000176.
XX
PR 21-MAY-2001; 2001GB-00012342.
XX
PA (GEMV-) GEMVAX AS.
XX
PI Eriksen JA, Gaudernack G, Moller M, Saeboe-Larssen S;
XX
DR WPI; 2003-129380/12.
XX
PT New polypeptides derived from human telomerase reverse transcriptase,
PT useful in preparing a medicament for treating or preventing cancer, or in
PT preparing a diagnostic for diagnosing cancer, e.g. breast cancer or
PT prostate cancer.
XX
PS Disclosure; Fig 2; 56pp; English.
XX
CC The present sequence represents a splice variant of a fragment of human
CC telomerase reverse transcriptase (hTERT). The specification describes
CC peptides derived from hTERT, which are capable of inducing a T cell
CC response and are used in medicine. The hTERT peptides and nucleic acids
CC encoding them are useful in preparing a medicament, which is a vaccine,
CC an antisense molecule, or is capable of generating an antisense molecule
CC in vivo, for treating cancer, or in preparing a diagnostic for diagnosing
CC cancer. The cancer is, for example, breast cancer, prostate cancer,
CC pancreatic cancer, colo-rectal cancer, lung cancer, malignant melanoma,
CC leukemia, lymphoma, ovarian cancer, cervical cancer, or a biliary tract
CC carcinoma
XX
SQ Sequence 174 AA;

  Query Match   11.2%; Score 667; DB 6; Length 174;
  Best Local Similarity   100.0%; Pred. No. 1.4e-47;
  Matches 130; Conservative   0; Mismatches   0; Indels   0; Gaps   0;

```
Qy        634 VNMDYVVGARTFRREKRAERLTSRVKALFSVLNYERARRPGLLGASVLGLDDIHRAWRTF 693
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 VNMDYVVGARTFRREKRAERLTSRVKALFSVLNYERARRPGLLGASVLGLDDIHRAWRTF 60
```

```
Qy        694 VLRVRAQDPPPELYFVKVDVTGAYDTIPQDRLTEVIASIIKPQNTYCVRRYAVVQKAAHG 753
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 VLRVRAQDPPPELYFVKVDVTGAYDTIPQDRLTEVIASIIKPQNTYCVRRYAVVQKAAHG 120

Qy        754 HVRKAFKSHV 763
              ||||||||||
Db        121 HVRKAFKSHV 130
```

RESULT 85
AAW97385
ID AAW97385 standard; protein; 131 AA.
XX
AC AAW97385;
XX
DT 14-MAY-1999 (first entry)
XX
DE Amino acid sequence of the specification.
XX
KW Catalytic telomerase; diagnosis; disease; telomerase activity.
XX
OS Homo sapiens.
XX
PN JP11046768-A.
XX
PD 23-FEB-1999.
XX
PF 01-AUG-1997; 97JP-00207708.
XX
PR 01-AUG-1997; 97JP-00207708.
XX
PA (MITU) MITSUBISHI CHEM CORP.
XX
DR WPI; 1999-208111/18.
DR N-PSDB; AAX15924.
XX
PT New catalytic protein of telomerase of a higher animal and a gene coding
PT it - useful for diagnosis of diseases caused by the change in activity of
PT a telomerase.
XX
PS Example 1; Page 14; 18pp; Japanese.
XX
CC The specification describes a human catalytic telomerase protein. The
CC products are useful in drug compositions for the diagnosis of diseases
CC caused by the change in activity of telomerase. The present sequence
CC appears in the specification
XX
SQ Sequence 131 AA;

  Query Match   10.9%; Score 651; DB 2; Length 131;
  Best Local Similarity   98.5%; Pred. No. 2.1e-46;
  Matches 128; Conservative   2; Mismatches   0; Indels   0; Gaps   0;

```
Qy        542 AKFLHWLMSVYVVELLRSFFYVTETTFQKNRLFFYRKSVWSKLQSIGIRQHLKRVQLREL 601
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||:::
Db          1 AKFLHWLMSVYVVELLRSFFYVTETTFQKNRLFFYRKSVWSKLQSIGIRQHLKRVQLRDV 60

Qy        602 SEAEVRQHREARPALLTSRLRFIPKPDGLRPIVNMDYVVGARTFRREKRAERLTSRVKAL 661
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 SEAEVRQHREARPALLTSRLRFIPKPDGLRPIVNMDYVVGARTFRREKRAERLTSRVKAL 120

Qy        662 FSVLNYERAR 671
              ||||||||||
Db        121 FSVLNYERAR 130
```

RESULT 86
AAW56107
ID AAW56107 standard; protein; 988 AA.
XX
AC AAW56107;
XX

```
DT   13-AUG-1998  (first entry)
XX
DE   S. pombe trt protein sequence designated tez1.
XX
KW   Human; telomerase reverse transcriptase; hTRT; TRT; diagnosis; prognosis;
KW   cell proliferation; cancer; ageing; ribonucleoprotein.
XX
OS   Schizosaccharomyces pombe.
XX
PN   GB2317891-A.
XX
PD   08-APR-1998.
XX
PF   01-OCT-1997;   97GB-00020890.
XX
PR   01-OCT-1996;   96US-00724643.
PR   18-APR-1997;   97US-00844419.
PR   25-APR-1997;   97US-00846017.
PR   06-MAY-1997;   97US-00851843.
PR   09-MAY-1997;   97US-00854050.
PR   14-AUG-1997;   97US-00911312.
PR   14-AUG-1997;   97US-00912951.
PR   14-AUG-1997;   97US-00915503.
XX
PA   (GERO-) GERON CORP.
PA   (UYTE-) UNIV TECHNOLOGY CORP.
XX
PI   Cech TR,  Lingner J,  Nakamura T,  Chapman KB,  Morin GB,  Harley CB;
PI   Andrews WH;
XX
DR   WPI; 1998-171633/16.
DR   N-PSDB; AAV22423.
XX
PT   Pure and recombinant human Telomerase Reverse Transcriptase and its
PT   variants - are useful in the diagnosis, prognosis and treatment of cell
PT   proliferation conditions especially cancer and ageing.
XX
PS   Example 1; Fig 51; 387pp; English.
XX
CC   The present sequence is Schizosaccharomyces pombe trt designated tez1
CC   from the present invention. The present invention also describes the
CC   following methods: (A) determining whether a test compound is a modulator
CC   of hTRT, by detecting the change in hTRT recombinant protein or
CC   polynucleotide, on administration of the compound; (B) preparation of
CC   recombinant telomerase by contacting a protein preparation of hTRT with a
CC   telomerase RNA component; (C) detection of the hTRT RNA or protein in a
CC   sample by binding a relevant probe to the sample and detecting the
CC   complex formed or in the case of RNA detection, amplifying the product
CC   and correlating the presence of complex or amplification product with
CC   presence of hTRT in the sample; and (D) increasing the proliferation of a
CC   vertebrate cell by increasing hTRT expression; and (E) the use of an
CC   agent that causes an increase in cell vertebrate cell proliferation to
CC   create a medicament that inhibits ageing. A protein preparation of hTRT
CC   and the polynucleotide encoding hTRT can be used in the manufacture of
CC   medicaments for inhibiting the effect of ageing or cancer. Inhibitors of
CC   telomerase activity can be used to treat conditions that are associated
CC   with high telomerase activity. A protein preparation of hTRT can also be
CC   used in the new methods
XX
SQ   Sequence 988 AA;

  Query Match             10.0%;  Score 594;  DB 2;  Length 988;
  Best Local Similarity   22.3%;  Pred. No. 2.3e-40;
  Matches  238;  Conservative  202;  Mismatches  379;  Indels  248;  Gaps   42;

Qy          5 PRCRAVRSLLRSHYREVLPLATFVRRLGPQGWRLVQRGDPAAFRALVAQCL--------- 55
              |: | :|  | : |  :  |  :|        :|| || ||:  : : : |
Db          7 PKSRILR-FLENQYVYLCTLNDYV--------QLVLRGSPASSYSNICERLRSDVQTSFS 57

Qy         56 -----VCVPWDARPPPAAPSFRQVSCLK-ELVARVLQRLCERG---AKNVLAFGFAL-LD 105
                    | :|::|      |    | : ||:| |:::: :      :|:|  ||::  :
Db         58 IFLHSTVVGFDSKPDEGV-QFSSPKCSQSELIANVVKQMFDESFERRRNLLMKGFSMNHE 116

Qy        106 GARGGPPEAFTTSVRSYLPNTVTDALRGSGAWGLLLRRVGDDVLVHLLARCALFVLVAPS 165
              |          : |  || :   |  |  | |||  :| | : :||:: ::|  :
Db        117 DFRAMHVNGVQNDLVSTFPNYLISILE-SKNWQLLLEIIGSDAMHYLLSKGSIFEALPND 175

Qy        166 CAYQVCGPPLYQLGAATQARPPPHASGPRRRLGCERAWNHSVREAGVPLGLPAPGARRRG 225
              |: | ||::                                ::| |  |        :::|
Db        176 NYLQISGIPLFK--------------------------NNVFEETV--------SKKRK 200

Qy        226 GSASRSLPLPKRPRRGAAPEPERTPVGQGSWAHPGRTRGPSDRGFCVVSPARPAEEATSL 285
              :   |:   |  |:           : ||
Db        201 RTIETSITQNKSARK-----------EVSW---------------------------- 219

Qy        286 EGALSGTRHS--HPSVGRQHHAGPPSTSRPPRPWDTPCPPVYAETKHF-LYSSGDKEQLR 342
              ::| :|  |  : |  ::                      : :  :| |:|  |:  :
Db        220 -NSISISRFSIFYRSSYKK--------------------FKQDLYFNLHSICDRNTVH 256

Qy        343 PSFLLSSLRPSLTG------ARRLVETIFLGSRPWMPGTPRRL----PRLPQRYWQMRPL 392
                |  : |   |        ::| : | | |:  :   |:||    | : |   ::  :
Db        257 --MWLQWIFPRQFGLINAFQVKQLHKVIPLVSQSTV--VPKRLLKVYPLIEQTAKRLHRI 312

Qy        393 FLELLGNHAQCPYGVLLKTHCPLRAAVTPAAGVCAREKPQGSVAAPEEEDTDPRRLVQLL 452
              |  : ||  |||   : ||                                ::|      ::|
Db        313 SLSKVYNH-YCPY---IDTH-------------------------DDE--------KIL 334

Qy        453 RQHSSPWQVYGFVRACLRRLVPPGLWGSRHNERRFLRNTKKFISLGKHAKLSLQELTWKM 512
                | ||: |:|: | |: |  :||::       |:: : |: | ::   ||  |   :
Db        335 SYSLKPNQVFAFLRSILVRVFPKLIWGNQRIFEIILKDLETFLKLSRYESFSLHYLMSNI 394

Qy        513 SVRDCAWL---RRSPGVGCVPAAEHRLREEILAKFLHWLMSVYVVELLRSFFYVTETTFQ 569
              : :  ||   :||    |:  ::   |::| |:|::|| : ::: :|:||||:||::
Db        395 KISEIEWLVLGKRSNAKMCL--SDFEKRKQIFAEFIYWLYNSFIIPILQSFFYITESSDL 452

Qy        570 KNRLFFYRKSVWSKLQSIGIRQHLKRVQLRELSEAEVRQHREARPALLTSRLRFIPKPDG 629
              :||  ::|| :| ||       :|     :::|  ||   : :  |  : :| :|| :
Db        453 RNRTVYFRKDIW-KLLCRPFITSMKMEAFEKINENNVRMDTQ-KTTLPPAVIRLLPKKNT 510

Qy        630 LRPIVNMDYVVGARTFRREKRAERLTSRVKALFSVLNYERARRP------GLLGASVLGL 683
              | | |:          |::   :: |  | | |     :  ||       |:     |:
Db        511 FRLITNL----------RKRFLIKMGSNKKMLVST---NQTLRPVASILKHLINEESSGI 557

Qy        684 D---DIHRAWRTF---VLRVRAQDPPPELYFVKVDVTGAYDTIPQDRLTEVIASIIKPQN 737
                ::    ||   :|: |       : |||::|:   || | || :  ::   :|
Db        558 PFNLEVYMKLLTFKKDLLKHRMFG--RKKYFVRIDIKSCYDRIKQDLMFRIVKKKLKDPE 615

Qy        738 TYCVRRYAVVQKAAHGHVRKAFKSHVSTLTDLQPYMRQFVAHLQETSPLRDAVVIEQSSS 797
              : :|:|| :  |       | | |   :  |: |: :       :||   | : ::
Db        616 -FVIRKYATIH-ATSDRATKNFVSEAFSYFDMVPFEKVVQLLSMKTS---DTLFVDFVDY 670

Qy        798 LNEASSGLFDVFLRFMCHHAVRIRGKSYVQCQGIPQGSILSTLLCSLCYGDMENKLFAGI 857
              ::|| :| :    :  | |:|     |:|  |||||||||: ||      |: ::  :
Db        671 WTKSSSEIFKMLKEHLSGHIVKIGNSQYLQKVGIPQGSILSSFLCHFYMEDLIDEYLSFT 730

Qy        858 RRDG-LLLRLVDDFLLVTPHLTHAKTFLRTLVRGVPEYGCVVNLRKTVVNFPVEDEALGG 916
              :: | :|||:|||| :| :   || ||   :||  ::    :| |||:||   :  :
Db        731 KKKGSVLLRVVDDFLFITVNKKDAKKFLNLSLRGFEKHNFSTSLEKTVINFENSNGIINN 790

Qy        917 TAFVQMPAHGLFPWCGLLLDTRTLEV-----QSDYSSYARTSIRASLTFNRGFKAGRNMR 971
              | | :       |: |  :: |:|:     : | : :  ||:  :    : |
Db        791 TFFNESKKR--MPFFGFSVNMRSLDTLLACPKIDEALFNSTSVELTKHMGKSF------- 841

Qy        972 RKLFGVLRLKCHS---LFLDLQVNSLQTVCTNIYKI-----LLLQAY 1010
              : :||     |   :|:|:  ||     | |||::     :  |||
Db        842 --FYKILRSSLASFAQVFIDITHNSKFNSCCNIYRLGYSMCMRAQAY 886


RESULT 87
ADG70135
ID   ADG70135 standard; protein; 816 AA.
XX
AC   ADG70135;
XX
DT   11-MAR-2004  (first entry)
XX
```

```
DE   HIV RT/hTERT chimeric construct #16.
XX
KW   cytostatic; gene therapy; reverse transcriptase-Inhibitor; HIV-1;
KW   human telomerase reverse transcriptase; hTERT; chimeric; catalytic site;
KW   unregulated cellular growth; cancer; tumor.
XX
OS   Chimeric.
OS   Homo sapiens.
OS   Human immunodeficiency virus 1.
XX
PN   WO2003095605-A2.
XX
PD   20-NOV-2003.
XX
PF   14-APR-2003; 2003WO-EP003874.
XX
PR   08-MAY-2002; 2002US-0378820P.
XX
PA   (PHAA ) PHARMACIA ITAL SPA.
XX
PI   Moll J,  Schnuchel A,  Stouten P;
XX
DR   WPI; 2004-012095/01.
XX
PT   New HIV-1 Reverse Transcriptase and human Telomerase Reverse
PT   Transcriptase proteins and nucleic acids, useful in gene therapy or for
PT   treating or preventing unregulated cellular growth, e.g. cancer cell or
PT   tumor growth.
XX
PS   Claim 1; SEQ ID NO 25; 141pp; English.
XX
CC   The invention relates to the isolation of compounds that bind and inhibit
CC   the activity of HIV-1 reverse transcriptase (RT) or human telomerase
CC   reverse transcriptase (hTERT). The method involves determining these
CC   compounds using a HIV-1 RT/hTERT chimeric construct containing the
CC   catalytic sites of each enzyme. The nucleic acid is useful for treating
CC   or preventing unregulated cellular growth, including cancer cell and
CC   tumor growth. It is also useful in gene therapy. Compounds that inhibit
CC   telomerase activity can be used to treat cancer. The vectors of the
CC   invention can be used to amplify DNA or RNA encoding HIV-RT/hTERT and/or
CC   express DNA which encodes HIV-RT/hTERT. This sequence corresponds to a
CC   chimeric HIV-RT/hTERT protein construct.
XX
SQ   Sequence 816 AA;

  Query Match             9.5%;  Score 565;  DB 8;  Length 816;
  Best Local Similarity   43.9%;  Pred. No. 4.9e-38;
  Matches  143;  Conservative   14;  Mismatches   33;  Indels  136;  Gaps   11;

Qy        624 IPKPDGLRPIVNMDYVVGARTFRR-EKRAERLTSRVKALFSVLNYERARRPGLLGASVLG 682
              | |||||| :|:          ||   || :
Db        303 IDKPDGLRKLVD---------FRELNKRTQDF---------------------------- 325

Qy        683 LDDIHRAWRTFVLRVRAQDPPPELYFVKVDVTGAYDTIPQDRLTEVIASIIKPQNTYCVR 742
              ||||||||||||||||||||||||||||||||| |                       |
Db        326 -------WRTFVLRVRAQDPPPELYFVKVDVTGAYDTIPWDE---------------DFR 363

Qy        743 RYAVVQKAAHGHVRKAFKSHVSTLTDLQPYMRQFVAHLQETSPLRDAVVIEQSSSLNEAS 802
              :|          ||              | |           |:|  :
Db        364 KYT-----------AF----------------------TIP----------SINNET 377

Qy        803 SGLFDVFLRFMCHHAVRIRGKSYVQCQGIPQG-----SILSTLLCSLCYGDMENKLFAGI 857
              |    :|:              |   :|||     :|  : :  :       : |
Db        378 PG-----IRY-------------QYNVLPQGWKGSPAIFQSSMTKIL------EPFKKQ 412

Qy        858 RRDGLLLRLVDDFLLVTPHLTHAKTFLRTLVRGVPEYGCVVNLRKTVVNFPVEDEALGGT 917
              | |||||||||||||||||||||||||||||||||| ||||||||||||||||||||||
Db        413 NPDILLLRLVDDFLLVTPHLTHAKTFLRTLVRGVPEYGSVVNLRKTVVNFPVEDEALGGT 472

Qy        918 AFVQMPAHGLFPWCGLLLDTRTLEVQ 943
              |||||||||||||||||||||||||
Db        473 AFVQMPAHGLFPWCGLLLDTRTLEVQ 498
```

```
RESULT 88
ADG70131
ID   ADG70131 standard; protein; 586 AA.
XX
AC   ADG70131;
XX
DT   11-MAR-2004  (first entry)
XX
DE   HIV RT/hTERT chimeric construct #12.
XX
KW   cytostatic; gene therapy; reverse transcriptase-Inhibitor; HIV-1;
KW   human telomerase reverse transcriptase; hTERT; chimeric; catalytic site;
KW   unregulated cellular growth; cancer; tumor.
XX
OS   Chimeric.
OS   Homo sapiens.
OS   Human immunodeficiency virus 1.
XX
PN   WO2003095605-A2.
XX
PD   20-NOV-2003.
XX
PF   14-APR-2003; 2003WO-EP003874.
XX
PR   08-MAY-2002; 2002US-0378820P.
XX
PA   (PHAA ) PHARMACIA ITAL SPA.
XX
PI   Moll J,  Schnuchel A,  Stouten P;
XX
DR   WPI; 2004-012095/01.
XX
PT   New HIV-1 Reverse Transcriptase and human Telomerase Reverse
PT   Transcriptase proteins and nucleic acids, useful in gene therapy or for
PT   treating or preventing unregulated cellular growth, e.g. cancer cell or
PT   tumor growth.
XX
PS   Claim 1; SEQ ID NO 21; 141pp; English.
XX
CC   The invention relates to the isolation of compounds that bind and inhibit
CC   the activity of HIV-1 reverse transcriptase (RT) or human telomerase
CC   reverse transcriptase (hTERT). The method involves determining these
CC   compounds using a HIV-1 RT/hTERT chimeric construct containing the
CC   catalytic sites of each enzyme. The nucleic acid is useful for treating
CC   or preventing unregulated cellular growth, including cancer cell and
CC   tumor growth. It is also useful in gene therapy. Compounds that inhibit
CC   telomerase activity can be used to treat cancer. The vectors of the
CC   invention can be used to amplify DNA or RNA encoding HIV-RT/hTERT and/or
CC   express DNA which encodes HIV-RT/hTERT. This sequence corresponds to a
CC   chimeric HIV-RT/hTERT protein construct.
XX
SQ   Sequence 586 AA;

  Query Match             9.3%;  Score 555;  DB 8;  Length 586;
  Best Local Similarity   43.6%;  Pred. No. 2.1e-37;
  Matches  142;  Conservative   14;  Mismatches   34;  Indels  136;  Gaps   11;

Qy        624 IPKPDGLRPIVNMDYVVGARTFRR-EKRAERLTSRVKALFSVLNYERARRPGLLGASVLG 682
              | |||||| :|:          ||   || :
Db         73 IDKPDGLRKLVD---------FRELNKRTQDF---------------------------- 95

Qy        683 LDDIHRAWRTFVLRVRAQDPPPELYFVKVDVTGAYDTIPQDRLTEVIASIIKPQNTYCVR 742
              ||||||||||||||||||||||||||||||||| |                       |
Db         96 -------WRTFVLRVRAQDPPPELYFVKVDVTGAYDTIPWDE---------------DFR 133

Qy        743 RYAVVQKAAHGHVRKAFKSHVSTLTDLQPYMRQFVAHLQETSPLRDAVVIEQSSSLNEAS 802
              :|          ||              | |           |:|  :
Db        134 KYT-----------AF----------------------TIP----------SINNET 147

Qy        803 SGLFDVFLRFMCHHAVRIRGKSYVQCQGIPQG-----SILSTLLCSLCYGDMENKLFAGI 857
              |    :|:              |   :|||     :|  : :  :       : |
Db        148 PG-----IRY-------------QYNVLPQGWKGSPAIFQSSMTKIL------EPFKKQ 182
```

```
Qy        858 RRDGLLLRLVDDFLLVTPHLTHAKTFLRTLVRGVPEYGCVVNLRKTVVNFPVEDEALGGT 917
              | ||||||||||||||||||||||||||||||||||||||| ||||||||||||||||||||
Db        183 NPDILLLRLVDDFLLVTPHLTHAKTFLRTLVRGVPEYGSVVNLRKTVVNFPVEDEALGGT 242

Qy        918 AFVQMPAHGLFPWCGLLLDTRTLEVQ 943
              ||||||||||||| ||||||||||||
Db        243 AFVQMPAHGLFPWSGLLLDTRTLEVQ 268


RESULT 89
ADG70134
ID   ADG70134 standard; protein; 803 AA.
XX
AC   ADG70134;
XX
DT   11-MAR-2004  (first entry)
XX
DE   HIV RT/hTERT chimeric construct #15.
XX
KW   cytostatic; gene therapy; reverse transcriptase-Inhibitor; HIV-1;
KW   human telomerase reverse transcriptase; hTERT; chimeric; catalytic site;
KW   unregulated cellular growth; cancer; tumor.
XX
OS   Chimeric.
OS   Homo sapiens.
OS   Human immunodeficiency virus 1.
XX
PN   WO2003095605-A2.
XX
PD   20-NOV-2003.
XX
PF   14-APR-2003; 2003WO-EP003874.
XX
PR   08-MAY-2002; 2002US-0378820P.
XX
PA   (PHAA ) PHARMACIA ITAL SPA.
XX
PI   Moll J,  Schnuchel A,  Stouten P;
XX
DR   WPI; 2004-012095/01.
XX
PT   New HIV-1 Reverse Transcriptase and human Telomerase Reverse
PT   Transcriptase proteins and nucleic acids, useful in gene therapy or for
PT   treating or preventing unregulated cellular growth, e.g. cancer cell or
PT   tumor growth.
XX
PS   Claim 1; SEQ ID NO 24; 141pp; English.
XX
CC   The invention relates to the isolation of compounds that bind and inhibit
CC   the activity of HIV-1 reverse transcriptase (RT) or human telomerase
CC   reverse transcriptase (hTERT). The method involves determining these
CC   compounds using a HIV-1 RT/hTERT chimeric construct containing the
CC   catalytic sites of each enzyme. The nucleic acid is useful for treating
CC   or preventing unregulated cellular growth, including cancer cell and
CC   tumor growth. It is also useful in gene therapy. Compounds that inhibit
CC   telomerase activity can be used to treat cancer. The vectors of the
CC   invention can be used to amplify DNA or RNA encoding HIV-RT/hTERT and/or
CC   express DNA which encodes HIV-RT/hTERT. This sequence corresponds to a
CC   chimeric HIV-RT/hTERT protein construct.
XX
SQ   Sequence 803 AA;

  Query Match             9.3%;  Score 555;  DB 8;  Length 803;
  Best Local Similarity   43.6%;  Pred. No. 3.4e-37;
  Matches  142;  Conservative   14;  Mismatches   34;  Indels  136;  Gaps   11;

Qy        624 IPKPDGLRPIVNMDYVVGARTFRR-EKRAERLTSRVKALFSVLNYERARRPGLLGASVLG 682
              | |||||| :|:         ||   || :
Db        290 IDKPDGLRKLVD---------FRELNKRTQDF--------------------------- 312

Qy        683 LDDIHRAWRTFVLRVRAQDPPPELYFVKVDVTGAYDTIPQDRLTEVIASIIKPQNTYCVR 742
                  |||||||||||||||||||||||||||||| |                 |
Db        313 -------WRTFVLRVRAQDPPPELYFVKVDVTGAYDTIPWDE--------------DFR 350

Qy        743 RYAVVQKAAHGHVRKAFKSHVSTLTDLQPYMRQFVAHLQETSPLRDAVVIEQSSSLNEAS 802
              :|          ||                 | |           |:| :
Db        351 KYT----------AF---------------------TIP----------SINNET 364

Qy        803 SGLFDVFLRFMCHHAVRIRGKSYVQCQGIPQG-----SILSTLLCSLCYGDMENKLFAGI 857
              |     :|:              |   :|||     :| : :  :       : |
Db        365 PG-----IRY-------------QYNVLPQGWKGSPAIFQSSMTKIL------EPFKKQ 399

Qy        858 RRDGLLLRLVDDFLLVTPHLTHAKTFLRTLVRGVPEYGCVVNLRKTVVNFPVEDEALGGT 917
              | ||||||||||||||||||||||||||||||||||||||| ||||||||||||||||||||
Db        400 NPDILLLRLVDDFLLVTPHLTHAKTFLRTLVRGVPEYGSVVNLRKTVVNFPVEDEALGGT 459

Qy        918 AFVQMPAHGLFPWCGLLLDTRTLEVQ 943
              ||||||||||||| ||||||||||||
Db        460 AFVQMPAHGLFPWSGLLLDTRTLEVQ 485


RESULT 90
ADG70133
ID   ADG70133 standard; protein; 816 AA.
XX
AC   ADG70133;
XX
DT   11-MAR-2004  (first entry)
XX
DE   HIV RT/hTERT chimeric construct #14.
XX
KW   cytostatic; gene therapy; reverse transcriptase-Inhibitor; HIV-1;
KW   human telomerase reverse transcriptase; hTERT; chimeric; catalytic site;
KW   unregulated cellular growth; cancer; tumor.
XX
OS   Chimeric.
OS   Homo sapiens.
OS   Human immunodeficiency virus 1.
XX
PN   WO2003095605-A2.
XX
PD   20-NOV-2003.
XX
PF   14-APR-2003; 2003WO-EP003874.
XX
PR   08-MAY-2002; 2002US-0378820P.
XX
PA   (PHAA ) PHARMACIA ITAL SPA.
XX
PI   Moll J,  Schnuchel A,  Stouten P;
XX
DR   WPI; 2004-012095/01.
XX
PT   New HIV-1 Reverse Transcriptase and human Telomerase Reverse
PT   Transcriptase proteins and nucleic acids, useful in gene therapy or for
PT   treating or preventing unregulated cellular growth, e.g. cancer cell or
PT   tumor growth.
XX
PS   Example 1; SEQ ID NO 23; 141pp; English.
XX
CC   The invention relates to the isolation of compounds that bind and inhibit
CC   the activity of HIV-1 reverse transcriptase (RT) or human telomerase
CC   reverse transcriptase (hTERT). The method involves determining these
CC   compounds using a HIV-1 RT/hTERT chimeric construct containing the
CC   catalytic sites of each enzyme. The nucleic acid is useful for treating
CC   or preventing unregulated cellular growth, including cancer cell and
CC   tumor growth. It is also useful in gene therapy. Compounds that inhibit
CC   telomerase activity can be used to treat cancer. The vectors of the
CC   invention can be used to amplify DNA or RNA encoding HIV-RT/hTERT and/or
CC   express DNA which encodes HIV-RT/hTERT. This sequence corresponds to a
CC   chimeric HIV-RT/hTERT protein construct.
XX
SQ   Sequence 816 AA;

  Query Match             9.3%;  Score 555;  DB 8;  Length 816;
```

```
  Best Local Similarity   43.6%;  Pred. No. 3.4e-37;
  Matches  142;  Conservative   14;  Mismatches   34;  Indels  136;  Gaps   11;

Qy        624 IPKPDGLRPIVNMDYVVGARTFRR-EKRAERLTSRVKALFSVLNYERARRPGLLGASVLG 682
              | |||||| :|:         ||   || :
Db        303 IDKPDGLRKLVD---------FRELNKRTQDF--------------------------- 325

Qy        683 LDDIHRAWRTFVLRVRAQDPPPELYFVKVDVTGAYDTIPQDRLTEVIASIIKPQNTYCVR 742
                  |||||||||||||||||||||||||||||| |                       |
Db        326 -------WRTFVLRVRAQDPPPELYFVKVDVTGAYDTIPWDE--------------DFR 363

Qy        743 RYAVVQKAAHGHVRKAFKSHVSTLTDLQPYMRQFVAHLQETSPLRDAVVIEQSSSLNEAS 802
              :|          ||                      | |           |:|  :
Db        364 KYT-----------AF----------------------TIP----------SINNET 377

Qy        803 SGLFDVFLRFMCHHAVRIRGKSYVQCQGIPQG-----SILSTLLCSLCYGDMENKLFAGI 857
              |     :|:              |   :|||     :|  : :  :       : |
Db        378 PG-----IRY-------------QYNVLPQGWKGSPAIFQSSMTKIL------EPFKKQ 412

Qy        858 RRDGLLLRLVDDFLLVTPHLTHAKTFLRTLVRGVPEYGCVVNLRKTVVNFPVEDEALGGT 917
                | |||||||||||||||||||||||||||||| ||||||||||||||||||||||
Db        413 NPDILLLRLVDDFLLVTPHLTHAKTFLRTLVRGVPEYGSVVNLRKTVVNFPVEDEALGGT 472

Qy        918 AFVQMPAHGLFPWCGLLLDTRTLEVQ 943
              |||||||||||| ||||||||||||
Db        473 AFVQMPAHGLFPWSGLLLDTRTLEVQ 498
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RESULT 91
ABB99682
ID   ABB99682 standard; protein; 108 AA.
XX
AC   ABB99682;
XX
DT   28-MAR-2003  (first entry)
XX
DE   Splice variant of a human telomerase reverse transcriptase fragment.
XX
KW   Human; telomerase reverse transcriptase; hTERT; T cell response; vaccine;
KW   cancer.
XX
OS   Homo sapiens.
XX
PN   WO200294312-A1.
XX
PD   28-NOV-2002.
XX
PF   16-MAY-2002; 2002WO-NO000176.
XX
PR   21-MAY-2001; 2001GB-00012342.
XX
PA   (GEMV-) GEMVAX AS.
XX
PI   Eriksen JA,  Gaudernack G,  Moller M,  Saeboe-Larssen S;
XX
DR   WPI; 2003-129380/12.
XX
PT   New polypeptides derived from human telomerase reverse transcriptase,
PT   useful in preparing a medicament for treating or preventing cancer, or in
PT   preparing a diagnostic for diagnosing cancer, e.g. breast cancer or
PT   prostate cancer.
XX
PS   Disclosure; Fig 2; 56pp; English.
XX
CC   The present sequence represents a splice variant of a fragment of human
CC   telomerase reverse transcriptase (hTERT). The specification describes
CC   peptides derived from hTERT, which are capable of inducing a T cell
CC   response and are used in medicine. The hTERT peptides and nucleic acids
CC   encoding them are useful in preparing a medicament, which is a vaccine,
CC   an antisense molecule, or is capable of generating an antisense molecule
CC   in vivo, for treating cancer, or in preparing a diagnostic for diagnosing
CC   cancer. The cancer is, for example, breast cancer, prostate cancer,
CC   pancreatic cancer, colo-rectal cancer, lung cancer, malignant melanoma,
CC   leukemia, lymphoma, ovarian cancer, cervical cancer, or a biliary tract
CC   carcinoma
XX
SQ   Sequence 108 AA;

  Query Match             9.0%;  Score 535;  DB 6;  Length 108;
  Best Local Similarity   90.0%;  Pred. No. 9.5e-37;
  Matches  108;  Conservative    0;  Mismatches    0;  Indels   12;  Gaps    1;

Qy        634 VNMDYVVGARTFRREKRAERLTSRVKALFSVLNYERARRPGLLGASVLGLDDIHRAWRTF 693
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 VNMDYVVGARTFRREKRAERLTSRVKALFSVLNYERARRPGLLGASVLGLDDIHRAWRTF 60

Qy        694 VLRVRAQDPPPELYFVKVDVTGAYDTIPQDRLTEVIASIIKPQNTYCVRRYAVVQKAAHG 753
              ||||||||||||||||||            ||||||||||||||||||||||||||||||
Db         61 VLRVRAQDPPPELYFVK------------DRLTEVIASIIKPQNTYCVRRYAVVQKAAHG 108
```

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RESULT 92
ABG71628
ID   ABG71628 standard; protein; 100 AA.
XX
AC   ABG71628;
XX
DT   09-JAN-2003  (first entry)
XX
DE   hTERT fragment with HLA containing polypeptide at its C-terminus.
XX
KW   Human; telomerase catalytic subunit; hTERT; human leukocyte antigen;
KW   human telomerase reverse transcriptase; HLA epitope; cancer; HLA profile;
KW   breast cancer; pancreatic cancer; colorectal cancer; lung cancer;
KW   ovarian cancer; cervical cancer; malignant melanoma; leukaemia; lymphoma;
KW   biliary tract carcinoma; anti-cancer; mutant; cytostatic;
KW   HLA class I epitope; HLA class II epitope; mutein.
XX
OS   Homo sapiens.
OS   Synthetic.
XX
PN   WO200270679-A2.
XX
PD   12-SEP-2002.
XX
PF   19-FEB-2002; 2002WO-NO000069.
XX
PR   02-MAR-2001; 2001GB-00005238.
XX
PA   (GEMV-) GEMVAX AS.
XX
PI   Eriksen JA,  Gaudernack G,  Moller M;
XX
DR   WPI; 2002-750459/81.
XX
PT   New polypeptide with an additional C-terminal and/or N-terminal sequence,
PT   useful for preparing anti-cancer vaccines.
XX
PS   Disclosure; Fig 2; 62pp; English.
XX
CC   The present invention relates to a polypeptide comprising a 20 amino acid
CC   sequence derived from human telomerase catalytic subunit (or human
CC   telomerase reverse transcriptase, hTERT) amino acid residues 537-556, or
CC   fragments thereof comprising at least 10 amino acids and at least two
CC   human leukocyte antigen (HLA) class I or class II epitopes. The invention
CC   also describes a polypeptide having the above 20 amino acid peptide
CC   sequence as additional C- and/or N-terminal sequences on a fragment of
CC   hTERT which is not more than 100 amino acids of hTERT. The polypeptides
CC   of the invention are useful in a pharmaceutical composition or in a
CC   vaccine for preventing or treating cancer in populations of individuals
CC   having varying HLA profiles. The polypeptides are also useful in a
CC   diagnostic kit for diagnosing cancers such as breast, pancreatic,
CC   colorectal, lung, ovarian or cervical cancer, malignant melanoma,
CC   leukaemia, lymphoma or biliary tract carcinoma. The polypeptides or
CC   encoding polynucleotide sequences are useful for performing identity,
CC   sequence homology and/or hybridisation studies, for predicting structure
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CC   and/or function (e.g. anti-cancer activity), or for screening methods in
CC   drug development or drug screening procedures. The present sequence
CC   represents a hTERT fragment with the 20 amino acid HLA epitope containing
CC   polypeptide at its C-terminus
XX
SQ   Sequence 100 AA;

  Query Match             9.0%;  Score 534;  DB 5;  Length 100;
  Best Local Similarity   98.0%;  Pred. No. 1e-36;
  Matches   98;  Conservative    1;  Mismatches    1;  Indels    0;  Gaps    0;

Qy        457 SPWQVYGFVRACLRRLVPPGLWGSRHNERRFLRNTKKFISLGKHAKLSLQELTWKMSVRD 516
              ||||||||||||||||||||||||||||||||||||||||||||||:||||||||||||
Db          1 SPWQVYGFVRACLRRLVPPGLWGSRHNERRFLRNTKKFISLGKHAKISLQELTWKMSVRG 60

Qy        517 CAWLRRSPGVGCVPAAEHRLREEILAKFLHWLMSVYVVEL 556
              |||||||||||||||||||||||||||||||||||||||
Db         61 CAWLRRSPGVGCVPAAEHRLREEILAKFLHWLMSVYVVEL 100


RESULT 93
ABG71627
ID   ABG71627 standard; protein; 100 AA.
XX
AC   ABG71627;
XX
DT   09-JAN-2003  (first entry)
XX
DE   hTERT fragment with HLA containing polypeptide at its N-terminus.
XX
KW   Human; telomerase catalytic subunit; hTERT; human leukocyte antigen;
KW   human telomerase reverse transcriptase; HLA epitope; cancer; HLA profile;
KW   breast cancer; pancreatic cancer; colorectal cancer; lung cancer;
KW   ovarian cancer; cervical cancer; malignant melanoma; leukaemia; lymphoma;
KW   biliary tract carcinoma; anti-cancer; mutant; cytostatic;
KW   HLA class I epitope; HLA class II epitope; mutein.
XX
OS   Homo sapiens.
OS   Synthetic.
XX
PN   WO200270679-A2.
XX
PD   12-SEP-2002.
XX
PF   19-FEB-2002; 2002WO-NO000069.
XX
PR   02-MAR-2001; 2001GB-00005238.
XX
PA   (GEMV-) GEMVAX AS.
XX
PI   Eriksen JA,  Gaudernack G,  Moller M;
XX
DR   WPI; 2002-750459/81.
XX
PT   New polypeptide with an additional C-terminal and/or N-terminal sequence,
PT   useful for preparing anti-cancer vaccines.
XX
PS   Disclosure; Fig 1; 62pp; English.
XX
CC   The present invention relates to a polypeptide comprising a 20 amino acid
CC   sequence derived from human telomerase catalytic subunit (or human
CC   telomerase reverse transcriptase, hTERT) amino acid residues 537-556, or
CC   fragments thereof comprising at least 10 amino acids and at least two
CC   human leukocyte antigen (HLA) class I or class II epitopes. The invention
CC   also describes a polypeptide having the above 20 amino acid peptide
CC   sequence as additional C- and/or N-terminal sequences on a fragment of
CC   hTERT which is not more than 100 amino acids of hTERT. The polypeptides
CC   of the invention are useful in a pharmaceutical composition or in a
CC   vaccine for preventing or treating cancer in populations of individuals
CC   having varying HLA profiles. The polypeptides are also useful in a
CC   diagnostic kit for diagnosing cancers such as breast, pancreatic,
CC   colorectal, lung, ovarian or cervical cancer, malignant melanoma,
CC   leukaemia, lymphoma or biliary tract carcinoma. The polypeptides or
CC   encoding polynucleotide sequences are useful for performing identity,
CC   sequence homology and/or hybridisation studies, for predicting structure
CC   and/or function (e.g. anti-cancer activity), or for screening methods in
CC   drug development or drug screening procedures. The present sequence
CC   represents a hTERT fragment with the 20 amino acid HLA epitope containing
CC   polypeptide at its N-terminus
XX
SQ   Sequence 100 AA;

  Query Match             8.5%;  Score 509;  DB 5;  Length 100;
  Best Local Similarity   100.0%;  Pred. No. 1.3e-34;
  Matches  100;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        537 REEILAKFLHWLMSVYVVELLRSFFYVTETTFQKNRLFFYRKSVWSKLQSIGIRQHLKRV 596
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 REEILAKFLHWLMSVYVVELLRSFFYVTETTFQKNRLFFYRKSVWSKLQSIGIRQHLKRV 60

Qy        597 QLRELSEAEVRQHREARPALLTSRLRFIPKPDGLRPIVNM 636
              ||||||||||||||||||||||||||||||||||||||||
Db         61 QLRELSEAEVRQHREARPALLTSRLRFIPKPDGLRPIVNM 100


RESULT 94
ADG70112
ID   ADG70112 standard; protein; 576 AA.
XX
AC   ADG70112;
XX
DT   11-MAR-2004  (first entry)
XX
DE   HIV-1 RT/hTERT chimera protein.
XX
KW   cytostatic; gene therapy; reverse transcriptase-Inhibitor; HIV-1;
KW   human telomerase reverse transcriptase; hTERT; chimeric; catalytic site;
KW   unregulated cellular growth; cancer; tumor.
XX
OS   Chimeric.
OS   Homo sapiens.
OS   Human immunodeficiency virus 1.
XX
PN   WO2003095605-A2.
XX
PD   20-NOV-2003.
XX
PF   14-APR-2003; 2003WO-EP003874.
XX
PR   08-MAY-2002; 2002US-0378820P.
XX
PA   (PHAA ) PHARMACIA ITAL SPA.
XX
PI   Moll J,  Schnuchel A,  Stouten P;
XX
DR   WPI; 2004-012095/01.
DR   N-PSDB; ADG70111.
XX
PT   New HIV-1 Reverse Transcriptase and human Telomerase Reverse
PT   Transcriptase proteins and nucleic acids, useful in gene therapy or for
PT   treating or preventing unregulated cellular growth, e.g. cancer cell or
PT   tumor growth.
XX
PS   Claim 1; SEQ ID NO 2; 141pp; English.
XX
CC   The invention relates to the isolation of compounds that bind and inhibit
CC   the activity of HIV-1 reverse transcriptase (RT) or human telomerase
CC   reverse transcriptase (hTERT). The method involves determining these
CC   compounds using a HIV-1 RT/hTERT chimeric construct containing the
CC   catalytic sites of each enzyme. The nucleic acid is useful for treating
CC   or preventing unregulated cellular growth, including cancer cell and
CC   tumor growth. It is also useful in gene therapy. Compounds that inhibit
CC   telomerase activity can be used to treat cancer. The vectors of the
CC   invention can be used to amplify DNA or RNA encoding HIV-RT/hTERT and/or
CC   express DNA which encodes HIV-RT/hTERT. This sequence corresponds to a
CC   chimeric HIV-RT/hTERT protein.
```

```
XX
SQ   Sequence 576 AA;

  Query Match             8.0%;  Score 478;  DB 8;  Length 576;
  Best Local Similarity   40.0%;  Pred. No. 6.4e-31;
  Matches  132;  Conservative   16;  Mismatches   38;  Indels  144;  Gaps   13;

Qy        624 IPKPDGLRPIVNMDYVVGARTFRREKRAERLTSRVKALFSVLNYERARRPGLLGASVLGL 683
              | |||||| :|:         ||       |  | :  : |                ||:
Db         63 IDKPDGLRKLVD---------FR------ELNKRTQDFWEV--------------QLGI 92

Qy        684 DDIHRAWRTFVLRVRAQDPPP-----ELYFVKVDVTGAYDTIPQDRLTEVIASIIKPQNT 738
                          | |       ||||||||||||||| |
Db         93 -----------------PHPAGLKKNGYFVKVDVTGAYDTIPWDE------------- 120

Qy        739 YCVRRYAVVQKAAHGHVRKAFKSHVSTLTDLQPYMRQFVAHLQETSPLRDAVVIEQSSSL 798
               |:|              ||                 | |           |:
Db        121 -DFRKYT-----------AF---------------------TIP----------SI 133

Qy        799 NEASSGLFDVFLRFMCHHAVRIRGKSYVQCQGIPQG-----SILSTLLCSLCYGDMENKL 853
              |  : |     :|:              |   :|||     :|  : :  :       :
Db        134 NNETPG-----IRY-------------QYNVLPQGWKGSPAIFQSSMTKIL------EP 168

Qy        854 FAGIRRDGLLLRLVDDFLLVTPHLTHAKTFLRTLVRGVPEYGCVVNLRKTVVNFPVEDEA 913
              |      | ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        169 FKKQNPDILLLRLVDDFLLVTPHLTHAKTFLRTLVRGVPEYGCVVNLRKTVVNFPVEDEA 228

Qy        914 LGGTAFVQMPAHGLFPWCGLLLDTRTLEVQ 943
              |||||||||||||||||||||||||||||
Db        229 LGGTAFVQMPAHGLFPWCGLLLDTRTLEVQ 258


RESULT 95
ADG70120
ID   ADG70120 standard; protein; 592 AA.
XX
AC   ADG70120;
XX
DT   11-MAR-2004  (first entry)
XX
DE   HIV RT/hTERT chimeric construct #1.
XX
KW   cytostatic; gene therapy; reverse transcriptase-Inhibitor; HIV-1;
KW   human telomerase reverse transcriptase; hTERT; chimeric; catalytic site;
KW   unregulated cellular growth; cancer; tumor.
XX
OS   Chimeric.
OS   Homo sapiens.
OS   Human immunodeficiency virus 1.
XX
PN   WO2003095605-A2.
XX
PD   20-NOV-2003.
XX
PF   14-APR-2003; 2003WO-EP003874.
XX
PR   08-MAY-2002; 2002US-0378820P.
XX
PA   (PHAA ) PHARMACIA ITAL SPA.
XX
PI   Moll J,  Schnuchel A,  Stouten P;
XX
DR   WPI; 2004-012095/01.
XX
PT   New HIV-1 Reverse Transcriptase and human Telomerase Reverse
PT   Transcriptase proteins and nucleic acids, useful in gene therapy or for
PT   treating or preventing unregulated cellular growth, e.g. cancer cell or
PT   tumor growth.
XX
PS   Example 1; SEQ ID NO 10; 141pp; English.
XX
CC   The invention relates to the isolation of compounds that bind and inhibit
CC   the activity of HIV-1 reverse transcriptase (RT) or human telomerase
CC   reverse transcriptase (hTERT). The method involves determining these
CC   compounds using a HIV-1 RT/hTERT chimeric construct containing the
CC   catalytic sites of each enzyme. The nucleic acid is useful for treating
CC   or preventing unregulated cellular growth, including cancer cell and
CC   tumor growth. It is also useful in gene therapy. Compounds that inhibit
CC   telomerase activity can be used to treat cancer. The vectors of the
CC   invention can be used to amplify DNA or RNA encoding HIV-RT/hTERT and/or
CC   express DNA which encodes HIV-RT/hTERT. This sequence corresponds to a
CC   chimeric HIV-RT/hTERT protein construct.
XX
SQ   Sequence 592 AA;

  Query Match             8.0%;  Score 478;  DB 8;  Length 592;
  Best Local Similarity   40.0%;  Pred. No. 6.6e-31;
  Matches  132;  Conservative   16;  Mismatches   38;  Indels  144;  Gaps   13;

Qy        624 IPKPDGLRPIVNMDYVVGARTFRREKRAERLTSRVKALFSVLNYERARRPGLLGASVLGL 683
              | |||||| :|:         ||       |  | :  : |                ||:
Db         79 IDKPDGLRKLVD---------FR------ELNKRTQDFWEV--------------QLGI 108

Qy        684 DDIHRAWRTFVLRVRAQDPPP-----ELYFVKVDVTGAYDTIPQDRLTEVIASIIKPQNT 738
                          | |       ||||||||||||||| |
Db        109 -----------------PHPAGLKKNGYFVKVDVTGAYDTIPWDE------------- 136

Qy        739 YCVRRYAVVQKAAHGHVRKAFKSHVSTLTDLQPYMRQFVAHLQETSPLRDAVVIEQSSSL 798
               |:|              ||                 | |           |:
Db        137 -DFRKYT-----------AF---------------------TIP----------SI 149

Qy        799 NEASSGLFDVFLRFMCHHAVRIRGKSYVQCQGIPQG-----SILSTLLCSLCYGDMENKL 853
              |  : |     :|:              |   :|||     :|  : :  :       :
Db        150 NNETPG-----IRY-------------QYNVLPQGWKGSPAIFQSSMTKIL------EP 184

Qy        854 FAGIRRDGLLLRLVDDFLLVTPHLTHAKTFLRTLVRGVPEYGCVVNLRKTVVNFPVEDEA 913
              |      | ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        185 FKKQNPDILLLRLVDDFLLVTPHLTHAKTFLRTLVRGVPEYGCVVNLRKTVVNFPVEDEA 244

Qy        914 LGGTAFVQMPAHGLFPWCGLLLDTRTLEVQ 943
              |||||||||||||||||||||||||||||
Db        245 LGGTAFVQMPAHGLFPWCGLLLDTRTLEVQ 274


RESULT 96
ADG70121
ID   ADG70121 standard; protein; 605 AA.
XX
AC   ADG70121;
XX
DT   11-MAR-2004  (first entry)
XX
DE   HIV RT/hTERT chimeric construct #2.
XX
KW   cytostatic; gene therapy; reverse transcriptase-Inhibitor; HIV-1;
KW   human telomerase reverse transcriptase; hTERT; chimeric; catalytic site;
KW   unregulated cellular growth; cancer; tumor.
XX
OS   Chimeric.
OS   Homo sapiens.
OS   Human immunodeficiency virus 1.
XX
PN   WO2003095605-A2.
XX
PD   20-NOV-2003.
XX
PF   14-APR-2003; 2003WO-EP003874.
XX
PR   08-MAY-2002; 2002US-0378820P.
XX
PA   (PHAA ) PHARMACIA ITAL SPA.
XX
PI   Moll J,  Schnuchel A,  Stouten P;
XX
DR   WPI; 2004-012095/01.
XX
```

```
PT   New HIV-1 Reverse Transcriptase and human Telomerase Reverse
PT   Transcriptase proteins and nucleic acids, useful in gene therapy or for
PT   treating or preventing unregulated cellular growth, e.g. cancer cell or
PT   tumor growth.
XX
PS   Example 1; SEQ ID NO 11; 141pp; English.
XX
CC   The invention relates to the isolation of compounds that bind and inhibit
CC   the activity of HIV-1 reverse transcriptase (RT) or human telomerase
CC   reverse transcriptase (hTERT). The method involves determining these
CC   compounds using a HIV-1 RT/hTERT chimeric construct containing the
CC   catalytic sites of each enzyme. The nucleic acid is useful for treating
CC   or preventing unregulated cellular growth, including cancer cell and
CC   tumor growth. It is also useful in gene therapy. Compounds that inhibit
CC   telomerase activity can be used to treat cancer. The vectors of the
CC   invention can be used to amplify DNA or RNA encoding HIV-RT/hTERT and/or
CC   express DNA which encodes HIV-RT/hTERT. This sequence corresponds to a
CC   chimeric HIV-RT/hTERT protein construct.
XX
SQ   Sequence 605 AA;

  Query Match             8.0%;  Score 478;  DB 8;  Length 605;
  Best Local Similarity   40.0%;  Pred. No. 6.8e-31;
  Matches  132;  Conservative   16;  Mismatches   38;  Indels  144;  Gaps   13;

Qy        624 IPKPDGLRPIVNMDYVVGARTFRREKRAERLTSRVKALFSVLNYERARRPGLLGASVLGL 683
              | |||||| :|:         ||        |  | :  : |                ||:
Db         79 IDKPDGLRKLVD---------FR------ELNKRTQDFWEV--------------QLGI 108

Qy        684 DDIHRAWRTFVLRVRAQDPPP-----ELYFVKVDVTGAYDTIPQDRLTEVIASIIKPQNT 738
                          | |       ||||||||||||||| |
Db        109 -----------------PHPAGLKKNGYFVKVDVTGAYDTIPWDE-------------- 136

Qy        739 YCVRRYAVVQKAAHGHVRKAFKSHVSTLTDLQPYMRQFVAHLQETSPLRDAVVIEQSSSL 798
                |:|             ||                       | |           |:
Db        137 -DFRKYT-----------AF----------------------TIP-----------SI 149

Qy        799 NEASSGLFDVFLRFMCHHAVRIRGKSYVQCQGIPQG-----SILSTLLCSLCYGDMENKL 853
              |  : |     :|:               |   :|||     :|  : :  :       :
Db        150 NNETPG-----IRY-------------QYNVLPQGWKGSPAIFQSSMTKIL------EP 184

Qy        854 FAGIRRDGLLLRLVDDFLLVTPHLTHAKTFLRTLVRGVPEYGCVVNLRKTVVNFPVEDEA 913
              |     | ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        185 FKKQNPDILLLRLVDDFLLVTPHLTHAKTFLRTLVRGVPEYGCVVNLRKTVVNFPVEDEA 244

Qy        914 LGGTAFVQMPAHGLFPWCGLLLDTRTLEVQ 943
              |||||||||||||||||||||||||||||
Db        245 LGGTAFVQMPAHGLFPWCGLLLDTRTLEVQ 274


RESULT 97
ADG70132
ID   ADG70132 standard; protein; 816 AA.
XX
AC   ADG70132;
XX
DT   11-MAR-2004  (first entry)
XX
DE   HIV RT/hTERT chimeric construct #13.
XX
KW   cytostatic; gene therapy; reverse transcriptase-Inhibitor; HIV-1;
KW   human telomerase reverse transcriptase; hTERT; chimeric; catalytic site;
KW   unregulated cellular growth; cancer; tumor.
XX
OS   Chimeric.
OS   Homo sapiens.
OS   Human immunodeficiency virus 1.
XX
PN   WO2003095605-A2.
XX
PD   20-NOV-2003.
XX
PF   14-APR-2003; 2003WO-EP003874.
XX
PR   08-MAY-2002; 2002US-0378820P.
XX
PA   (PHAA ) PHARMACIA ITAL SPA.
XX
PI   Moll J,  Schnuchel A,  Stouten P;
XX
DR   WPI; 2004-012095/01.
XX
PT   New HIV-1 Reverse Transcriptase and human Telomerase Reverse
PT   Transcriptase proteins and nucleic acids, useful in gene therapy or for
PT   treating or preventing unregulated cellular growth, e.g. cancer cell or
PT   tumor growth.
XX
PS   Claim 1; SEQ ID NO 22; 141pp; English.
XX
CC   The invention relates to the isolation of compounds that bind and inhibit
CC   the activity of HIV-1 reverse transcriptase (RT) or human telomerase
CC   reverse transcriptase (hTERT). The method involves determining these
CC   compounds using a HIV-1 RT/hTERT chimeric construct containing the
CC   catalytic sites of each enzyme. The nucleic acid is useful for treating
CC   or preventing unregulated cellular growth, including cancer cell and
CC   tumor growth. It is also useful in gene therapy. Compounds that inhibit
CC   telomerase activity can be used to treat cancer. The vectors of the
CC   invention can be used to amplify DNA or RNA encoding HIV-RT/hTERT and/or
CC   express DNA which encodes HIV-RT/hTERT. This sequence corresponds to a
CC   chimeric HIV-RT/hTERT protein construct.
XX
SQ   Sequence 816 AA;

  Query Match             7.7%;  Score 461;  DB 8;  Length 816;
  Best Local Similarity   39.9%;  Pred. No. 2.8e-29;
  Matches  131;  Conservative   15;  Mismatches   42;  Indels  140;  Gaps   13;

Qy        624 IPKPDGLRPIVNMDYVVGARTFRREKRAERLTSRVKALFSVLNYERARRPGLLGASVLGL 683
              | |||||| :|:         ||        |  | :  : |                ||:
Db        303 IDKPDGLRKLVD---------FR------ELNKRTQDFWEV--------------QLGI 332

Qy        684 DDIHRAWRTFVLRVRAQDPPP-----ELYFVKVDVTGAYDTIPQDRLTEVIASIIKPQNT 738
                          | |       ||||||||||||||| |
Db        333 -----------------PHPAGLKKNGYFVKVDVTGAYDTIPWDE-------------- 360

Qy        739 YCVRRYAVVQKAAHGHVRKAFKSHVSTLTDLQPYMRQFVAHLQETSPLRDAVVIEQSSSL 798
                |:|             ||                       | |           |:
Db        361 -DFRKYT-----------AF----------------------TIP-----------SI 373

Qy        799 NEASSGLFDVFLRFMCHHAVRIRGKSYVQCQGIPQGSILSTLLCSLCYGDMENKLFAGIR 858
              |  : |     :|:               |   :|||   |  :    :     |:   |
Db        374 NNETPG-----IRY-------------QYNVLPQGWKGSPAI----FQSSMTKILEPFR 410

Qy        859 R---DGLLLRLVDDFLLVTPHLTHAKTFLRTLVRGVPEYGCVVNLRKTVVNFPVEDEALG 915
              :   | |||||||||||||||||||||||||||||||||| ||||||||||||||||||
Db        411 KQNPDILLLRLVDDFLLVTPHLTHAKTFLRTLVRGVPEYGSVVNLRKTVVNFPVEDEALG 470

Qy        916 GTAFVQMPAHGLFPWCGLLLDTRTLEVQ 943
              |||||||||||||| ||||||||||||
Db        471 GTAFVQMPAHGLFPWSGLLLDTRTLEVQ 498


RESULT 98
ADG70126
ID   ADG70126 standard; protein; 456 AA.
XX
AC   ADG70126;
XX
DT   11-MAR-2004  (first entry)
XX
DE   HIV RT/hTERT chimeric construct #7.
XX
KW   cytostatic; gene therapy; reverse transcriptase-Inhibitor; HIV-1;
KW   human telomerase reverse transcriptase; hTERT; chimeric; catalytic site;
KW   unregulated cellular growth; cancer; tumor.
XX
```

OS Chimeric.
OS Homo sapiens.
OS Human immunodeficiency virus 1.
XX
PN WO2003095605-A2.
XX
PD 20-NOV-2003.
XX
PF 14-APR-2003; 2003WO-EP003874.
XX
PR 08-MAY-2002; 2002US-0378820P.
XX
PA (PHAA) PHARMACIA ITAL SPA.
XX
PI Moll J, Schnuchel A, Stouten P;
XX
DR WPI; 2004-012095/01.
XX
PT New HIV-1 Reverse Transcriptase and human Telomerase Reverse
PT Transcriptase proteins and nucleic acids, useful in gene therapy or for
PT treating or preventing unregulated cellular growth, e.g. cancer cell or
PT tumor growth.
XX
PS Example 1; SEQ ID NO 16; 141pp; English.
XX
CC The invention relates to the isolation of compounds that bind and inhibit
CC the activity of HIV-1 reverse transcriptase (RT) or human telomerase
CC reverse transcriptase (hTERT). The method involves determining these
CC compounds using a HIV-1 RT/hTERT chimeric construct containing the
CC catalytic sites of each enzyme. The nucleic acid is useful for treating
CC or preventing unregulated cellular growth, including cancer cell and
CC tumor growth. It is also useful in gene therapy. Compounds that inhibit
CC telomerase activity can be used to treat cancer. The vectors of the
CC invention can be used to amplify DNA or RNA encoding HIV-RT/hTERT and/or
CC express DNA which encodes HIV-RT/hTERT. This sequence corresponds to a
CC chimeric HIV-RT/hTERT protein construct.
XX
SQ Sequence 456 AA;

Query Match 7.7%; Score 459; DB 8; Length 456;
Best Local Similarity 39.4%; Pred. No. 1.8e-29;
Matches 130; Conservative 17; Mismatches 39; Indels 144; Gaps 13;

```
Qy        624 IPKPDGLRPIVNMDYVVGARTFRREKRAERLTSRVKALFSVLNYERARRPGLLGASVLGL 683
              | |||||| :|:         ||       |  | :  : |                ||:
Db         73 IDKPDGLRKLVD---------FR------ELNKRTQDFWEV--------------QLGI 102

Qy        684 DDIHRAWRTFVLRVRAQDPPP-----ELYFVKVDVTGAYDTIPQDRLTEVIASIIKPQNT 738
                                  | |     : |||||||||||||| |
Db        103 -----------------PHPAGLKKKGYFVKVDVTGAYDTIPWDE-------------- 130

Qy        739 YCVRRYAVVQKAAHGHVRKAFKSHVSTLTDLQPYMRQFVAHLQETSPLRDAVVIEQSSSL 798
                |:|              ||                    | |           |:
Db        131 -DFRKYT-----------AF----------------------TIP----------SI 143

Qy        799 NEASSGLFDVFLRFMCHHAVRIRGKSYVQCQGIPQG-----SILSTLLCSLCYGDMENKL 853
              |  : |     :|:              |   :|||     :|  : :  :       :
Db        144 NNETPG-----IRY-------------QYNVLPQGWKGSPAIFQSSMTKIL------EP 178

Qy        854 FAGIRRDGLLLRLVDDFLLVTPHLTHAKTFLRTLVRGVPEYGCVVNLRKTVVNFPVEDEA 913
              |      | |||||||||||||||||||||||||||||||||| ||||||||||||||||
Db        179 FKKQNPDILLLRLVDDFLLVTPHLTHAKTFLRTLVRGVPEYGSVVNLRKTVVNFPVEDEA 238

Qy        914 LGGTAFVQMPAHGLFPWCGLLLDTRTLEVQ 943
              |||||||||||||||| ||||||||||||
Db        239 LGGTAFVQMPAHGLFPWSGLLLDTRTLEVQ 268
```

RESULT 99
ADG70124
ID ADG70124 standard; protein; 462 AA.
XX
AC ADG70124;
XX
DT 11-MAR-2004 (first entry)
XX
DE HIV RT/hTERT chimeric construct #5.
XX
KW cytostatic; gene therapy; reverse transcriptase-Inhibitor; HIV-1;
KW human telomerase reverse transcriptase; hTERT; chimeric; catalytic site;
KW unregulated cellular growth; cancer; tumor.
XX
OS Chimeric.
OS Homo sapiens.
OS Human immunodeficiency virus 1.
XX
PN WO2003095605-A2.
XX
PD 20-NOV-2003.
XX
PF 14-APR-2003; 2003WO-EP003874.
XX
PR 08-MAY-2002; 2002US-0378820P.
XX
PA (PHAA) PHARMACIA ITAL SPA.
XX
PI Moll J, Schnuchel A, Stouten P;
XX
DR WPI; 2004-012095/01.
XX
PT New HIV-1 Reverse Transcriptase and human Telomerase Reverse
PT Transcriptase proteins and nucleic acids, useful in gene therapy or for
PT treating or preventing unregulated cellular growth, e.g. cancer cell or
PT tumor growth.
XX
PS Example 1; SEQ ID NO 14; 141pp; English.
XX
CC The invention relates to the isolation of compounds that bind and inhibit
CC the activity of HIV-1 reverse transcriptase (RT) or human telomerase
CC reverse transcriptase (hTERT). The method involves determining these
CC compounds using a HIV-1 RT/hTERT chimeric construct containing the
CC catalytic sites of each enzyme. The nucleic acid is useful for treating
CC or preventing unregulated cellular growth, including cancer cell and
CC tumor growth. It is also useful in gene therapy. Compounds that inhibit
CC telomerase activity can be used to treat cancer. The vectors of the
CC invention can be used to amplify DNA or RNA encoding HIV-RT/hTERT and/or
CC express DNA which encodes HIV-RT/hTERT. This sequence corresponds to a
CC chimeric HIV-RT/hTERT protein construct.
XX
SQ Sequence 462 AA;

Query Match 7.7%; Score 459; DB 8; Length 462;
Best Local Similarity 39.4%; Pred. No. 1.9e-29;
Matches 130; Conservative 17; Mismatches 39; Indels 144; Gaps 13;

```
Qy        624 IPKPDGLRPIVNMDYVVGARTFRREKRAERLTSRVKALFSVLNYERARRPGLLGASVLGL 683
              | |||||| :|:         ||       |  | :  : |                ||:
Db         79 IDKPDGLRKLVD---------FR------ELNKRTQDFWEV--------------QLGI 108

Qy        684 DDIHRAWRTFVLRVRAQDPPP-----ELYFVKVDVTGAYDTIPQDRLTEVIASIIKPQNT 738
                                  | |     : |||||||||||||| |
Db        109 -----------------PHPAGLKKKGYFVKVDVTGAYDTIPWDE-------------- 136

Qy        739 YCVRRYAVVQKAAHGHVRKAFKSHVSTLTDLQPYMRQFVAHLQETSPLRDAVVIEQSSSL 798
                |:|              ||                    | |           |:
Db        137 -DFRKYT-----------AF----------------------TIP----------SI 149

Qy        799 NEASSGLFDVFLRFMCHHAVRIRGKSYVQCQGIPQG-----SILSTLLCSLCYGDMENKL 853
              |  : |     :|:              |   :|||     :|  : :  :       :
Db        150 NNETPG-----IRY-------------QYNVLPQGWKGSPAIFQSSMTKIL------EP 184

Qy        854 FAGIRRDGLLLRLVDDFLLVTPHLTHAKTFLRTLVRGVPEYGCVVNLRKTVVNFPVEDEA 913
              |      | |||||||||||||||||||||||||||||||||| ||||||||||||||||
Db        185 FKKQNPDILLLRLVDDFLLVTPHLTHAKTFLRTLVRGVPEYGSVVNLRKTVVNFPVEDEA 244

Qy        914 LGGTAFVQMPAHGLFPWCGLLLDTRTLEVQ 943
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                ||||||||||||||||| ||||||||||||
Db        245 LGGTAFVQMPAHGLFPWSGLLLDTRTLEVQ 274
```

```
RESULT 100
ADG70123
ID   ADG70123 standard; protein; 592 AA.
XX
AC   ADG70123;
XX
DT   11-MAR-2004  (first entry)
XX
DE   HIV RT/hTERT chimeric construct #4.
XX
KW   cytostatic; gene therapy; reverse transcriptase-Inhibitor; HIV-1;
KW   human telomerase reverse transcriptase; hTERT; chimeric; catalytic site;
KW   unregulated cellular growth; cancer; tumor.
XX
OS   Chimeric.
OS   Homo sapiens.
OS   Human immunodeficiency virus 1.
XX
PN   WO2003095605-A2.
XX
PD   20-NOV-2003.
XX
PF   14-APR-2003; 2003WO-EP003874.
XX
PR   08-MAY-2002; 2002US-0378820P.
XX
PA   (PHAA ) PHARMACIA ITAL SPA.
XX
PI   Moll J,  Schnuchel A,  Stouten P;
XX
DR   WPI; 2004-012095/01.
XX
PT   New HIV-1 Reverse Transcriptase and human Telomerase Reverse
PT   Transcriptase proteins and nucleic acids, useful in gene therapy or for
PT   treating or preventing unregulated cellular growth, e.g. cancer cell or
PT   tumor growth.
XX
PS   Example 1; SEQ ID NO 13; 141pp; English.
XX
CC   The invention relates to the isolation of compounds that bind and inhibit
CC   the activity of HIV-1 reverse transcriptase (RT) or human telomerase
CC   reverse transcriptase (hTERT). The method involves determining these
CC   compounds using a HIV-1 RT/hTERT chimeric construct containing the
CC   catalytic sites of each enzyme. The nucleic acid is useful for treating
CC   or preventing unregulated cellular growth, including cancer cell and
CC   tumor growth. It is also useful in gene therapy. Compounds that inhibit
CC   telomerase activity can be used to treat cancer. The vectors of the
CC   invention can be used to amplify DNA or RNA encoding HIV-RT/hTERT and/or
CC   express DNA which encodes HIV-RT/hTERT. This sequence corresponds to a
CC   chimeric HIV-RT/hTERT protein construct.
XX
SQ   Sequence 592 AA;
```

```
  Query Match             7.7%;  Score 459;  DB 8;  Length 592;
  Best Local Similarity   39.4%;  Pred. No. 2.6e-29;
  Matches  130;  Conservative   17;  Mismatches   39;  Indels  144;  Gaps   13;

Qy        624 IPKPDGLRPIVNMDYVVGARTFRREKRAERLTSRVKALFSVLNYERARRPGLLGASVLGL 683
              | |||||| :|:         ||        |  | :  : |                ||:
Db         79 IDKPDGLRKLVD---------FR------ELNKRTQDFWEV--------------QLGI 108

Qy        684 DDIHRAWRTFVLRVRAQDPPP-----ELYFVKVDVTGAYDTIPQDRLTEVIASIIKPQNT 738
                          | |     : ||||||||||||||| |
Db        109 ------------------PHPAGLKKKGYFVKVDVTGAYDTIPWDE-------------- 136

Qy        739 YCVRRYAVVQKAAHGHVRKAFKSHVSTLTDLQPYMRQFVAHLQETSPLRDAVVIEQSSSL 798
                |:|             ||                        | |          |:
Db        137 -DFRKYT-----------AF----------------------TIP----------SI 149
```

```
Qy        799 NEASSGLFDVFLRFMCHHAVRIRGKSYVQCQGIPQG-----SILSTLLCSLCYGDMENKL 853
              |  : |     :|:              |   :|||     :|  : :  :       :
Db        150 NNETPG-----IRY-------------QYNVLPQGWKGSPAIFQSSMTKIL------EP 184

Qy        854 FAGIRRDGLLLRLVDDFLLVTPHLTHAKTFLRTLVRGVPEYGCVVNLRKTVVNFPVEDEA 913
              |     | |||||||||||||||||||||||||||||||| ||||||||||||||||
Db        185 FKKQNPDILLLRLVDDFLLVTPHLTHAKTFLRTLVRGVPEYGSVVNLRKTVVNFPVEDEA 244

Qy        914 LGGTAFVQMPAHGLFPWCGLLLDTRTLEVQ 943
              |||||||||||||||| ||||||||||||
Db        245 LGGTAFVQMPAHGLFPWSGLLLDTRTLEVQ 274
```

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Search completed: January 13, 2005, 15:52:40
Job time : 124 secs
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